

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:39:22 ; Search time 49 Seconds  
(without alignments)  
2056.099 Million cell updates/sec

Title: US-10-031-146-2  
Perfect score: 1048  
Sequence: 1 TIKEMPOKTFGEKLNPL.....RLWLQLEKGRYAKDVWAG 1048  
Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR-73.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	1049	1 A34286	NADPH-ferrihemopro
2	28	2.7	1054	1 A69975	NADPH-ferrihemopro
3	21	2.0	1061	2 D69799	Cytochrome P450 /
4	16	1.5	661	2 T40056	nadh-cytochrome p
5	16	1.5	678	1 S29123	NADPH-ferrihemopro
6	15	1.4	693	1 S38427	NADPH-ferrihemopro
7	13	1.2	558	2 T37567	probable NADPH cyt
8	13	1.2	605	1 G70040	sulfite reductase
9	13	1.2	607	2 A83726	sulfite reductase
10	13	1.2	710	2 JC7192	NADPH-ferrihemopro
11	12	1.1	677	1 RDPG04	NADPH-ferrihemopro
12	12	1.1	677	2 A60557	NADPH-ferrihemopro
13	12	1.1	678	2 S27158	NADPH-ferrihemopro
14	12	1.1	679	2 A25505	NADPH-ferrihemopro
15	12	1.1	691	1 S46735	NADPH-ferrihemopro
16	11	1.0	506	2 S37156	NADPH-ferrihemopro
17	11	1.0	681	2 T14903	NADPH-ferrihemopro
18	11	1.0	690	2 A47298	NADPH-ferrihemopro
19	11	1.0	692	2 T05582	NADPH-ferrihemopro
20	11	1.0	692	2 S37159	NADPH-ferrihemopro
21	11	1.0	693	2 T14904	NADPH-ferrihemopro
22	10	1.0	238	2 T10771	NADPH-ferrihemopro
23	10	1.0	571	2 T39378	probable FAD bindi
24	10	1.0	590	2 S37157	NADPH-ferrihemopro
25	10	1.0	601	2 A28577	NADPH-ferrihemopro
26	10	1.0	612	2 G82674	NADPH-sulfite redu
27	10	1.0	614	2 B82329	sulfite reductase
28	10	1.0	683	2 T10720	NADPH-ferrihemopro
29	10	1.0	1429	2 JN0609	nitric-oxide synth

30	10	1.0	1429	2 S16233	nitric-oxide synth
31	10	1.0	1433	2 G01946	nitric-oxide synth
32	9	0.9	327	2 S53305	ferredoxin-NADP re
33	9	0.9	375	2 T02215	ferredoxin-NADP re
34	9	0.9	378	1 T03758	probable ferredoxi
35	9	0.9	489	2 T06715	probable cytochrom
36	9	0.9	671	2 A56592	NADPH-ferrihemopro
37	9	0.9	680	2 S63895	NADPH-ferrihemopro
38	9	0.9	680	2 S63698	NADPH-ferrihemopro
39	9	0.9	680	2 A37890	NADPH-ferrihemopro
40	9	0.9	705	2 T10723	NADPH-ferrihemopro
41	9	0.9	1144	1 A43271	nitric-oxide synth
42	9	0.9	1147	1 S47647	nitric-oxide synth
43	9	0.9	1147	1 T56575	nitric-oxide synth
44	9	0.9	1147	1 S38253	nitric-oxide synth
45	9	0.9	1147	1 T53165	nitric-oxide synth

ALIGNMENTS

RESULT 1

A34286

NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Bacillus megaterium  
N:Contains: NADPH-ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (C:Species: Bacillus megaterium  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
C:Accession: A34286; S43653

R:Ruettinger, R.T.; Wen, L.P.; Fulco, A.J.  
J. Biol. Chem. 264, 10987-10995, 1989

A:Title: Coding nucleotide, 5' regulatory, and deduced amino acid sequences of P-450-

A:Reference number: A34286; MUID:89291834; PMID:2544578

A:Accession: A34286

A:Molecule type: DNA

A:Residues: 1-1049 <RUE>

A:Cross-references: GB:J04832; NID:g142797; PIDN:AAA87602.1; PID:g142798

R:Munro, A.W.; Lindsay, J.G.; Coggins, J.R.; Kelly, S.M.; Price, N.C.

FEBS Lett. 343, 70-74, 1994

A:Title: Structural and enzymological analysis of the interaction of isolated domains  
A:Reference number: S43653; MUID:94215710; PMID:8163021

A:Accession: S43653

A:Molecule type: protein

A:Residues: 430-439; 441-496 <MUN>

C:Genetics:

A:Gene: CYP102

C:Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin  
C:Keywords: chromoprotein; electron transfer; FAD; flavoprotein; FMN; heme; iron; met

F:262-423/Domain: cytochrome P450 homology <P45>

F:483-1046/Domain: NADPH-ferrihemoprotein reductase homology <FEH>

F:485-622/Domain: flavodoxin homology <FLX>

F:401/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 1048; DB 1; Length 1049;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIKEMPOKTFGEKLNPLNTDKPVQALMKIADLGELGFEKFEAPGRVTRVYLSORLIKE 60

Db 2 TIREMPOKTFGEKLNPLNTDKPVQALMKIADLGELGFEKFEAPGRVTRVYLSORLIKE 61

Qy 61 ACDESREDFKNLSQALKFVRDFAGDGLFTSWTHENKWKKAHNILLPSFSQAMKGYHAMV 120

Db 62 ACDESREDFKNLSQALKFVRDFAGDGLFTSWTHENKWKKAHNILLPSFSQAMKGYHAMV 121

Qy 121 DIAVOLQVKWERLNADHEIEVPEDMTRLTLDTIGLCGFNRYFNFSYRQDPHPFITSVMRA 180

Db 122 DIAVOLQVKWERLNADHEIEVPEDMTRLTLDTIGLCGFNRYFNFSYRQDPHPFITSVMRA 181

Qy 181 LDEAMNKLQRPNDPPAYDENKRFQEDIKVMNDLVKIIADRKASGEQSDLLTHMLNG 240

Db 182 LDEAMNKLQRPNDPPAYDENKRFQEDIKVMNDLVKIIADRKASGEQSDLLTHMLNG 241

Qy 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKPNHVLQKAAEAARLVLD 300

Db 242 KDPETGEPLDENIRYQITFLAGHETTSGLSFALYFLVKNPHYLKAAEEAARVLVD 301  
QY 301 PVPYSYQVQKLVGVMLNEALRLWTPAFSLYAKEDIVLGGEXPLEKGDDELWLIPOL 360  
Db 302 PVPYSYQVQKLVGVMLNEALRLWTPAFSLYAKEDIVLGGEXPLEKGDDELWLIPOL 361  
QY 361 HRDKTIWDDVEFRPERFENPSPAIPOHAFKPFNGQORACIGQOFALHEATLVGLMMLKH 420  
Db 362 HRDKTIWDDVEFRPERFENPSPAIPOHAFKPFNGQORACIGQOFALHEATLVGLMMLKH 421  
QY 421 FDPEDHTNYELDKETITLKPEGVVYKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 480  
Db 422 FDPEDHTNYELDKETITLKPEGVVYKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 481  
QY 481 PLLVLVGSNMGTAEGTARDLADTAMSGKFAPOQVATLDSHAGNLPREGAVLIVTASNGHP 540  
Db 482 PLLVLVGSNMGTAEGTARDLADTAMSGKFAPOQVATLDSHAGNLPREGAVLIVTASNGHP 541  
QY 541 PDNAKQFVWLQDQASADEYKGVYRVSFGCGDKNMWATYQKVPFADITETLAAGAENIADR 600  
Db 542 PDNAKQFVWLQDQASADEYKGVYRVSFGCGDKNMWATYQKVPFADITETLAAGAENIADR 601  
QY 601 GEADASDDDEGTVEEHRHWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 660  
Db 602 GEADASDDDEGTVEEHRHWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 661  
QY 661 AFSTNVVASKELQPGQASRSTRLEIETLPKEASQEGDHLGVIPRNYEGIVNRVTAFFGL 720  
Db 662 AFSTNVVASKELQPGQASRSTRLEIETLPKEASQEGDHLGVIPRNYEGIVNRVTAFFGL 721  
QY 721 DASQQLRLAEKLAHLPLAKTVSVVEILLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780  
Db 722 DASQQLRLAEKLAHLPLAKTVSVVEILLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781  
QY 781 EALLEKQAKQVLAERLWLELLEKYPACEMKFEFIALLSIRPRYYSISSSPVDEK 840  
Db 782 EALLEKQAKQVLAERLWLELLEKYPACEMKFEFIALLSIRPRYYSISSSPVDEK 841  
QY 841 QASITSVVSGEAWSGYGYKGIASNYLAELQEGDITCFISPPQSEFTLPKDPETPLIM 900  
Db 842 QASITSVVSGEAWSGYGYKGIASNYLAELQEGDITCFISPPQSEFTLPKDPETPLIM 901  
QY 901 VPGTGVAPFGRGVQARKQKQSGSLGSAHLVFGCRSPHEDYLYQEELENAQSEGIITL 960  
Db 902 VPGTGVAPFGRGVQARKQKQSGSLGSAHLVFGCRSPHEDYLYQEELENAQSEGIITL 961  
QY 961 HTAFSRMPNPKTYVQHVMEQDGKLLIELLDQGAHFYICGDSQMAPAVETILMKSADY 1020  
Db 962 HTAFSRMPNPKTYVQHVMEQDGKLLIELLDQGAHFYICGDSQMAPAVETILMKSADY 1021  
QY 1021 HQVSEADARLWLQOLEKGRYAKDVWAG 1048  
Db 1022 HQVSEADARLWLQOLEKGRYAKDVWAG 1049

## RESULT 2

A69975  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Bacillus subtilis  
N:Contains: NADPH-ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (EC  
C:Species: Bacillus subtilis  
C:Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 03-Jun-2002  
C:Accession: A69975  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,  
J. ;

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se  
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili  
F:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: A69975  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1054 <KUN>  
A:Cross-references: GB:299117; GB:AL009126; NID:G2634966; PID:G2635162  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yrhJ  
C:Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin  
C:Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein; monooxygenase; o  
F:486-1030/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F:488-625/Domain: flavodoxin homology <FLX>  
F:403/Binding site: heme iron (Cys) (axial ligand) #status predicted  
Query Match 2.7% Score 28; DB 1; Length 1054;  
Best Local Similarity 100.0%; Pred. No. 1.5e-18;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 249 LDENIRYQITFLIAGHETTSGLSFA 276  
Db 252 LDENIRYQITFLIAGHETTSGLSFA 279  
RESULT 3  
D69799  
cytochrome P450 / NADPH-cytochrome P450 r homolog yeto - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 28-Jul-2000  
C:Accession: D69799  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau  
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scan  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se  
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili  
F:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: D69799  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1061 <KUN>  
A:Cross-references: GB:299107; GB:AL009126; NID:G2632866; PID:G2632866; PID:G26330  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yeto  
C:Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin  
C:Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein  
F:264-425/Domain: cytochrome P450 homology <P45>  
F:493-1057/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F:495-632/Domain: flavodoxin homology <FLX>  
F:403/Binding site: heme iron (Cys) (axial ligand) #status predicted  
Query Match 2.0% Score 21; DB 2; Length 1061;  
Best Local Similarity 100.0%; Pred. No. 1.2e-11;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 144 DMTRLTDTIGLCGNGYRNS 164  
Db 146 DMTRLTDTIGLCGNGYRNS 166

## RESULT 4

T40056  
nadh-cytochrome p450 reductase - fission yeast (Schizosaccharomyces pombe) (fragment)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jun-2000  
C;Accession: T40056  
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lelaure, V.; Galibert, F.  
submitted to the EMBL Data Library, December 1998  
A;Reference number: Z21903  
A;Accession: T40056  
A;Status: preliminary;  
A;Molecule type: DNA  
A;Residues: 1-661 <LYN>  
A;Cross-references: EMBL:AL034463; PIDN:CAA22429.1; GSPDB:GN00067; SPDB:SPBC29A10.01  
A;Experimental source: strain 972h-; cosmid c29A10  
C;Genetics:  
A;Gene: SPDB:SPBC29A10.01  
A;Map position: 2  
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase; flavoprotein  
C;Keywords: flavoprotein

Query Match 1.5%; Score 16; DB 2; Length 661;

Best Local Similarity 100.0%; Pred. No. 6.7e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGGTGVAPFRGFV 914

|||||

Db 517 IMVPGGTGVAPFRGFV 532

## RESULT 5

S29123  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - fission yeast (Schizosaccharomyces pombe)  
N;Alternate names: NADP-cytochrome P450 reductase  
C;Species: Schizosaccharomyces pombe  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
C;Accession: S29123; S20134; R20814  
R;Miles, J.S.  
Biochem. J. 287, 195-200, 1992  
A;Title: Structurally and functionally conserved regions of cytochrome P-450 reductase a  
saccharomyces pombe cDNA.  
A;Reference number: S29123; MUID:93038553; PMID:1417773  
A;Accession: S29123  
A;Molecule type: mRNA  
A;Residues: 1-678 <MIL>  
A;Cross-references: EMBL:X64702; NID:g4943; PIDN:CAA45956.1; PID:g4944  
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lelaure, V.; Galibert, F.  
submitted to the EMBL Data Library, June 1999  
A;Reference number: Z21920  
A;Accession: T40324  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-678 <WOO>  
A;Cross-references: EMBL:AL078627; PIDN:CAB44769.1; GSPDB:GN00067; SPDB:SPBC365.17  
A;Experimental source: strain 972h-; cosmid c365  
C;Genetics:  
A;Gene: SPBC365.17  
A;Map position: 2  
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase; electron transfer; endoplasmic reticulum; FAD; flavoprotein; FMN; membrane F  
F;53-677/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F;55-208/Domain: flavodoxin homology <FLX>

Query Match 1.5%; Score 16; DB 1; Length 678;

Best Local Similarity 100.0%; Pred. No. 6.9e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGGTGVAPFRGFV 914

|||||

Db 534 IMVPGGTGVAPFRGFV 549

## RESULT 6

S38427  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger  
N;Alternate names: NADPH-cytochrome P450 oxidoreductase  
C;Species: Aspergillus niger  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
C;Accession: S38427  
R;van den Brink, J.; van Zeijl, C.; van den Hondel, C.; van Gorcom, R.  
submitted to the EMBL Data Library, October 1993  
A;Description: Cloning and characterization of the NADPH cytochrome P450 oxidoreducta  
A;Reference number: S38427  
A;Accession: S38427  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-693 <VAN>  
A;Cross-references: EMBL:Z26938; NID:g408110; PIDN:CAA81550.1; PID:g408111  
C;Genetics:  
A;Introns: 595/3  
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase; flavoprotein; NADP; oxidoreductase  
C;Keywords: NADPH-ferrihemoprotein reductase homology <FEH>  
F;66-691/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F;68-220/Domain: flavodoxin homology <FLX>

Query Match 1.4%; Score 15; DB 1; Length 693;

Best Local Similarity 100.0%; Pred. No. 6.8e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGGTGVAPFRGF 913

|||||

Db 544 IMVPGGTGVAPFRGF 558

## RESULT 7

T37567  
probable NADPH cytochrome reductase - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
C;Accession: T37567  
R;Wood, V.; Barrell, B.G.; Rajandream, M.A.; Harris, D.; Seeger, K.  
submitted to the EMBL Data Library, February 1999  
A;Reference number: Z21725  
A;Accession: T37567  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-558 <WOO>  
A;Cross-references: EMBL:AL035439; PIDN:CAB36512.2; GSPDB:GN00066; SPDB:SPAC1296.06  
A;Experimental source: strain 972h-; cosmid c1296  
C;Genetics:  
A;Gene: SPDB:SPAC1296.06  
A;Map position: 1  
A;Introns: 45/3; 71/3; 111/2  
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase; flavoprotein

Query Match 1.2%; Score 13; DB 2; Length 558;

Best Local Similarity 100.0%; Pred. No. 0.00052;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 897 PLIMVPGGTGVAP 909

|||||

Db 414 PLIMVPGGTGVAP 426

## RESULT 8

G70040  
sulfite reductase (NADPH2) (EC 1.8.1.2) flavoprotein yvgr - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
C;Accession: G70040  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Avevedo, V.; Ber  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen-  
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y, M.; Ogawa, K.; Ogiwara, K.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: G70040  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-605 <KUN>  
A:Cross-references: GB:299121; GB:AL009126; NID:g2635827; PIDN:CABL5349.1; PID:g2635857  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yvgr  
C:Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH-ferrihemoprotein re  
C:Keywords: flavoprotein; NADP; oxidoreductase  
F:58-604/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F:70-209/Domain: flavodoxin homology <FLX>

Query Match 1.2%; Score 13; DB 1; Length 605;  
Best Local Similarity 100.0%; Pred. No. 0.00056;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVGPCTGVAPFR 911  
Db 462 IMVGPCTGVAPFR 474  
|||||

RESULT 9  
A83726  
sulfite reductase (NADPH) BH0609 [Imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 03-May-2002  
C:Accession: A83726  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: A83726  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-607 <STO>  
A:Cross-references: GB:AP001509; GB:BA000004; NID:gl0173176; PIDN:BA04328.1; GSPDB:GN0  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH0609  
C:Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH-ferrihemoprotein re  
C:Keywords: flavoprotein

Query Match 1.2%; Score 13; DB 2; Length 607;  
Best Local Similarity 100.0%; Pred. No. 0.00057;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVGPCTGVAPFR 911  
Db 464 IMVGPCTGVAPFR 476  
|||||

RESULT 10  
JC7192  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Cunninghamella elegans  
C:Species: Cunninghamella elegans  
C:Date: 03-Nov-2000 #sequence\_revision 03-Nov-2000 #text\_change 03-Jun-2002  
C:Accession: JC7192  
R:Yadav, J.S.; Loper, J.C.  
Biochem. Biophys. Res. Commun. 268, 345-353, 2000

A:Title: Cloning and characterization of the cytochrome P450 oxidoreductase gene from  
A:Reference number: JC7192; MUID:20145435; PMID:10679206  
A:Accession: JC7192  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-710 <YAD>  
A:Cross-references: GB:AF195659  
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo  
C:Keywords: flavoprotein; oxidoreductase

Query Match 1.2%; Score 13; DB 2; Length 710;  
Best Local Similarity 100.0%; Pred. No. 0.00065;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 902 GPGTGVAPRGRFV 914  
Db 564 GPGTGVAPRGRFV 576  
|||||

RESULT 11  
RDPG04  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - pig  
N:Alternate names: NADP-cytochrome P450 reductase  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 04-Dec-1986 #sequence\_revision 03-Feb-1994 #text\_change 03-Jun-2002  
C:Accession: A25584; A00403  
R:Haniu, M.; Iyanagi, T.; Miller, P.; Lee, T.D.; Shively, J.E.  
Biochemistry 25, 7906-7911, 1986  
A:Title: Complete amino acid sequence of NADPH-cytochrome P-450 reductase from porcine  
A:Reference number: A25584; MUID:87101085; PMID:3099837  
A:Accession: A25584  
A:Molecule type: protein  
A:Residues: 1-677 <HAN>  
R:Voegel, F.; Lumper, L.  
Biochem. J. 236, 871-878, 1986  
A:Title: Complete structure of the hydrophilic domain in the porcine NADPH-cytochrome  
A:Reference number: A00403; MUID:87075664; PMID:3098240  
A:Accession: A00403  
A:Molecule type: protein  
A:Residues: 56-162 'S', 164-173 'D', 175-338 'A', 340-377 'D', 379-399 'E', 401-445 'L', 44  
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo  
C:Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; flav  
F:76-126/Domain: FMN binding <FMN>  
F:79-675/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F:81-223/Domain: flavodoxin homology <FLX>  
F:451-476/Domain: FAD binding <FAD>  
F:1/Modified site: acetylated amino end (Gly) #status experimental

Query Match 1.1%; Score 12; DB 1; Length 677;  
Best Local Similarity 100.0%; Pred. No. 0.006;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVGPCTGVAPF 910  
Db 528 IMVGPCTGVAPF 539  
|||||

RESULT 12  
A60557  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - human  
N:Alternate names: NADP-cytochrome P450 reductase  
C:Species: Homo sapiens (man)  
C:Date: 17-Apr-1993 #sequence\_revision 31-Dec-1993 #text\_change 03-Jun-2002  
C:Accession: A33421; A60557; S21686  
R:Haniu, M.; McManus, M.E.; Birkett, D.J.; Lee, T.D.; Shively, J.E.  
Biochemistry 28, 8639-8645, 1989  
A:Title: Structural and functional analysis of NADPH-cytochrome P-450 reductase from  
A:Reference number: A33421; MUID:90105390; PMID:2513880  
A:Accession: A33421  
A:Molecule type: protein  
A:Residues: 2-677 <HAN>  
A:Note: 551-Gln was also found  
R:Yamano, S.; Aoyama, T.; McBride, O.W.; Hardwick, J.P.; Gelboin, H.V.; Gonzalez, F.J



RESULT 14

A25505  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - rabbit  
C:Species: *Oryctolagus cuniculus* (domestic rabbit)  
C:Date: 05-Oct-1988 #sequence\_revision 05-Oct-1988 #text\_change 03-Jun-2002  
C:Accession: A25505; A05233  
R:Katagiri, M.; Murakami, H.; Yabasaki, Y.; Sugiyama, T.; Okamoto, M.; Yamano, T.; Oh, H.  
J. Biochem. 100, 945-954, 1986  
A:Title: Molecular cloning and sequence analysis of full-length cDNA for rabbit liver  
A:Reference number: A25505; MUID:87137361; PMID:3029050  
A:Accession: A25505  
A:Molecule type: mRNA  
A:Residues: 1-679 <RAT>  
A:Cross-references: GB:X04610; NID:g1543; PIDN:CAA28279.1; PID:g1544  
R:Black, S.D.; Coon, M.J.  
J. Biol. Chem. 257, 5925-5938, 1982  
A:Title: Structural features of liver microsomal NADPH-cytochrome P-450 reductase. Hy  
A:Reference number: A05233; MUID:82167456; PMID:6802823  
A:Accession: A05233  
A:Molecule type: protein  
A:Residues: 'PTHDG', 14-39, 'NY', 42-52, 'N', 54-81 <BLA>  
A:Note: the order of the first four residues was not determined  
A:Note: the amino end of the mature protein is acetylated  
C:Comment: This enzyme, a membrane-bound flavoprotein containing one molecule each of  
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihem  
C:Keywords: acetylated amino end; electron transfer; FAD; flavoprotein; FMN; membrane  
F:1-56/Domain: membrane-bound #status predicted <MEM>  
F:78-228/Domain: FMN binding #status predicted <FMN>  
F:81-677/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F:83-225/Domain: flavodoxin homology <FLX>  
F:85-96/Region: FMN-phosphate binding #status predicted  
F:268-327, 453-478/Domain: FAD binding #status predicted <FAD>  
F:294-297/Region: FAD-pyrophosphate binding #status predicted

Query Match 1.1%; Score 12; DB 2; Length 679;  
Best Local Similarity 100.0%; Pred. No. 0.006;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGGTGVAPF 910  
|||||  
DB 530 IMVPGGTGVAPF 541

RESULT 15

S46735  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - yeast (*Saccharomyces cerevisiae*)  
N:Alternate names: NADP-cytochrome P450 reductase; protein YHR042w  
C:Species: *Saccharomyces cerevisiae*  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
C:Accession: S46735; A14447; B41447  
R:Du, Z.  
submitted to the EMBL Data Library, May 1994  
A:Description: The sequence of *S. cerevisiae* cosmid 8179.  
A:Reference number: S46732  
A:Accession: S46735  
A:Molecule type: DNA  
A:Residues: 1-691 <DUZ>  
A:Cross-references: EMBL:U00062; NID:g488162; PIDN:AA68904.1; PID:g488169; GSPDB:GNO  
R:Yabasaki, Y.; Murakami, H.; Ohkawa, H.  
J. Biochem. 103, 1004-1010, 1988  
A:Title: Primary structure of *Saccharomyces cerevisiae* NADPH-cytochrome P450 reductas  
A:Reference number: A14447; MUID:89008184; PMID:3139648  
A:Accession: A14447  
A:Molecule type: DNA  
A:Residues: 1-422, 'N', 424-473, 'G', 475-691 <YAB>  
A:Cross-references: GB:D13788; GB:D00316; NID:g218452; PIDN:BA02936.1; PID:g218453  
A:Accession: B41447  
A:Molecule type: protein  
A:Residues: 2-13, 45-62 <YA2>  
C:Genetics:  
A:Gene: SGD:NCPl; PRD1; SGD:S0001084  
A:Cross-references: MIPS:YHR042w; SGD:S0001084  
A:Map position: 8R

C;Function:  
A;Description: electron transfer; oxidoreductase  
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase  
C;Keywords: electron transfer; endoplasmic reticulum; flavoprotein; NADP; oxidoreductase  
F;61-690/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F;63-204/Domain: flavodoxin homology <FLX>

Query Match 1.1%; Score 12; DB 1; Length 691;  
Best Local Similarity 100.0%; Pred. No. 0.0061;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 902 GPGTGVAPRGRF 913  
Db 540 GPGTGVAPRGRF 551  
|||||

Search completed: May 29, 2003, 08:44:50  
Job time : 50 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:32:22 ; Search time 26 Seconds  
(without alignments)  
1671.815 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 1048

Sequence: 1 TIKEMPQKTFGELKNLPL.....RLWLOEEKGRYAKDVGWAG 1048

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	1048	1	CPXB_BACME
2	28	2.7	1054	1	CYPE_BACSU
3	21	2.0	1061	1	CYPD_BACSU
4	16	1.5	678	1	NCPR_SCHPO
5	12	1.1	676	1	NCPR_HUMAN
6	12	1.1	677	1	NCPR_CAVPO
7	12	1.1	677	1	NCPR_MOUSE
8	12	1.1	677	1	NCPR_PIG
9	12	1.1	679	1	NCPR_RABIT
10	12	1.1	690	1	NCPR_YEAST
11	11	1.0	690	1	NCPR_PHAAT
12	10	1.0	571	1	YB63_SCHPO
13	10	1.0	601	1	NCPR_SALTR
14	10	1.0	1429	1	NOS1_MOUSE
15	10	1.0	1429	1	NOS1_RAT
16	10	1.0	1434	1	NOS1_HUMAN
17	10	1.0	1435	1	NOS1_RABIT
18	9	0.9	375	1	FENS_TOBAC
19	9	0.9	378	1	FENS_ORYSA
20	9	0.9	489	1	C71Q_ARATH
21	9	0.9	496	1	NOS2_RABIT
22	9	0.9	516	1	C4AD_DROME
23	9	0.9	671	1	NCPR_MUSDO
24	9	0.9	679	1	NCPR_DROME
25	9	0.9	680	1	NCPR_CANNA
26	9	0.9	680	1	NCPR_CANTR
27	9	0.9	1144	1	NOS2_MOUSE
28	9	0.9	1147	1	NOS2_RAT
29	9	0.9	1147	1	NS2D_HUMAN
30	9	0.9	1149	1	NS2D_CAVPO
31	9	0.9	1153	1	NOS_LYNST
32	8	0.8	200	1	VATE_BORBU
33	8	0.8	218	1	CP3J_CAPAE

RESULT 1  
CPXB\_BACME  
ID CPXB\_BACME STANDARD; PRT; 1048 AA.  
AC P14779;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Bifunctional P-450:NADPH-P450 reductase (Cytochrome P450(BM-3))  
DE (P450BM-3) [Includes: Cytochrome P450 102 (EC 1.14.14.1); NADPH-  
DE cytochrome P450 reductase (EC 1.6.2.4)].  
GN CYP102A1 OR CYP102.  
OS Bacillus megaterium.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99291834; PubMed=2544578;  
RA Ruettinger R.T., Wen L.-P., Fulco A.J.;  
RT "Coding nucleotide, 5' regulatory, and deduced amino acid sequences  
RT of P-450BM-3, a single peptide cytochrome P-450:NADPH-P-450  
RT reductase from Bacillus megaterium.";  
RL J. Biol. Chem. 264:10987-10995(1989).  
RN [2]  
RP CHARACTERIZATION.  
RX MEDLINE=92088245; PubMed=1727637;  
RA Boddupalli S.S., Pramanik B.C., Slaughter C.A., Estabrook R.W.,  
RA Peterson J.A.;  
RT "Fatty acid monooxygenation by P450BM-3: product identification and  
RT proposed mechanisms for the sequential hydroxylation reactions.";  
RL Arch. Biochem. Biophys. 292:20-28(1992).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-471.  
RX MEDLINE=93342510; PubMed=8342039;  
RA Ravichandran K.G., Boddupalli S.S., Hasemann C.A., Peterson J.A.,  
RA Deisenhofer J.;  
RT "Crystal structure of hemoprotein domain of P450BM-3, a prototype for  
RT microsomal P450 s.";  
RL Science 261:731-736(1993).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-471.  
RX MEDLINE=97185914; PubMed=9033595;  
RA Li H.Y., Poulos T.L.;  
RT "The structure of the cytochrome P450BM-3 haem domain complexed with  
RT the fatty acid substrate, palmitoleic acid.";  
RL Nat. Struct. Biol. 4:140-146(1997).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.03 ANGSTROMS) OF 1-458 AND 459-649.  
RX MEDLINE=99162523; PubMed=10051560;  
RA Sevriloukova I.F., Li H., Zhang H., Peterson J.A., Poulos T.L.;  
RT "Structure of a cytochrome P450-redox partner electron-transfer  
RT complex.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:1863-1868(1999).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS) OF 1-470.  
RX MEDLINE=2152924; PubMed=11695892;  
RA Haines D.C., Tomchick D.R., Machius M., Peterson J.A.;

34 Y556\_SYNY3 218 0.8 8  
35 ANKH\_CHRVI 323 0.8 8  
36 TMPB\_TREPA 325 0.8 8  
37 RADA\_PYPAB 356 0.8 8  
38 C13B\_XYLFA 402 0.8 8  
39 CPXE\_STRGO 405 0.8 8  
40 CPXH\_STRGR 412 0.8 8  
41 SYC\_RHIME 466 0.8 8  
42 CP35\_HUMAN 502 0.8 8  
43 YZ2R\_AGRVI 502 0.8 8  
44 C72R\_ARATH 503 0.8 8  
45 CP39\_RAT 503 0.8 8

#### ALIGNMENTS

RT Pivotal role of water in the mechanism of P450BM-3.  
 RL Biochemistry 40:13456-13465(2001).  
 CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. CATALYSES  
 CC HYDROXYLATION OF MEDIUM AND LONG-CHAIN FATTY ACIDS AT OMEGA-1,  
 CC OMEGA-2 AND OMEGA-3 POSITIONS, WITH OPTIMUM CHAIN LENGTHS OF 14-16  
 CC CARBONS (LAURIC, MYRISTIC, AND PALMITIC ACIDS). THE REDUCTASE  
 CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME  
 CC P450.  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
 CC ferrocyclochrome.  
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
 CC oxidized flavoprotein + H(2)O.  
 CC -1- COFACTOR: FAD AND FMN.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME  
 CC P450 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----

DR EMBL; J04832; AA87602.1;  
 DR PIR; A34286; A34286.  
 DR PDB; 2HPD; 31-OCT-93.  
 DR PDB; 2BMH; 31-JUL-94.  
 DR PDB; 1FAG; 12-FEB-97.  
 DR PDB; 1FAH; 12-FEB-97.  
 DR PDB; 1BU7; 23-SEP-98.  
 DR PDB; 1BYI; 23-FEB-99.  
 DR PDB; 1JPZ; 09-NOV-01.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR InterPro; IPR003097; FAD binding.  
 DR InterPro; IPR001709; FPN\_cyt\_redtase.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00067; p450; 1.  
 DR Pfam; PF00175; NAD\_binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR PRINTS; PR00371; FPNCR.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 DR Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
 KW Multifunctional enzyme; FMN; FAD; Flavoprotein; 3D-structure; NADP.  
 FT INIT MET 0  
 FT DOMAIN 0 471  
 FT BINDING 472 1048  
 FT DOMAIN 400 400  
 FT TURN 12 13  
 FT TURN 15 16  
 FT HELIX 17 20  
 FT HELIX 25 36  
 FT STRAND 39 44  
 FT TURN 45 46  
 FT STRAND 47 52  
 FT HELIX 55 61  
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 FT STRAND 139 140  
 FT HELIX 141 158

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 Query Match 100.0%; Score 1048; DB 1; Length 1048;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TIKEMPQKTFGELKNLPLNTDKPVQALMKIADLGEIFKFEAPGRVTRYLSSQRLIKE 60  
 DB 1 TIKEMPQKTFGELKNLPLNTDKPVQALMKIADLGEIFKFEAPGRVTRYLSSQRLIKE 60  
 QY 61 ACDESREFDKNLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPSFSQQAAMGYHAMV 120  
 DB 61 ACDESREFDKNLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPSFSQQAAMGYHAMV 120  
 QY 121 DIAVOLVQKWERLNADEHIEVPEDMTRTLTLDTIGLCGFNYRNFNSFYRQPHPTTSMVRA 180  
 DB 121 DIAVOLVQKWERLNADEHIEVPEDMTRTLTLDTIGLCGFNYRNFNSFYRQPHPTTSMVRA 180  
 QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIIADRKASGQSDDLLTHMLNG 240  
 DB 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIIADRKASGQSDDLLTHMLNG 240  
 QY 241 KPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARLVLD 300  
 DB 241 KPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARLVLD 300  
 QY 301 PVPSYKQVKQKLYVGMVNLNEALRLWPTAPAFSLAKEDTVLGGEYPLEKGDLMVLIIPQL 360  
 DB 301 PVPSYKQVKQKLYVGMVNLNEALRLWPTAPAFSLAKEDTVLGGEYPLEKGDLMVLIIPQL 360  
 QY 361 HRDKTIWGDDVVEEPRPERFENPSAIPQHAFFPGNGQRACIGQQQFALHEATLVLGMLKH 420  
 DB 361 HRDKTIWGDDVVEEPRPERFENPSAIPQHAFFPGNGQRACIGQQQFALHEATLVLGMLKH 420  
 QY 421 FDFEDHTNYELDIKETLTCLKPEGFVVKAKSKIPLGGIPSPSTEQSAKVKRKAENAHNT 480  
 DB 421 FDFEDHTNYELDIKETLTCLKPEGFVVKAKSKIPLGGIPSPSTEQSAKVKRKAENAHNT 480

Db 421 DFEDHTNYELDIKETITLTKPEGVVVKAKSKTILGIPSPSTEQSAKVRKAENAHNT 480  
QY 481 PLVLVGSNMGTAEGTARDLADLAMSQFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540  
Db 481 PLVLVGSNMGTAEGTARDLADLAMSQFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540  
QY 541 PDNAKQFVWLQDQASADEVKGVRYSVFGCGDKNWTYYQKVPAFIDETLAAKGAENIADR 600  
Db 541 PDNAKQFVWLQDQASADEVKGVRYSVFGCGDKNWTYYQKVPAFIDETLAAKGAENIADR 600  
QY 601 GEADASDDPEGTYEERHWSVDAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 660  
Db 601 GEADASDDPEGTYEERHWSVDAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 660  
QY 661 AFSTNVVASKELQPGCSARSTRLELPEKASQYQGDHGLGVIPRNYEGVIVNVRTARFGL 720  
Db 661 AFSTNVVASKELQPGCSARSTRLELPEKASQYQGDHGLGVIPRNYEGVIVNVRTARFGL 720  
QY 721 DASQQIRLEAEKLAHLPLAKTVSVVEELLQYVELQDPTVTRTOLRAMAAKTVCPPHKVEL 780  
Db 721 DASQQIRLEAEKLAHLPLAKTVSVVEELLQYVELQDPTVTRTOLRAMAAKTVCPPHKVEL 780  
QY 781 EALLEKQAYKEQVLAKRLMLELEKYPACEMKFSEFIALLPSIRPRYYSISSPRVDEK 840  
Db 781 EALLEKQAYKEQVLAKRLMLELEKYPACEMKFSEFIALLPSIRPRYYSISSPRVDEK 840  
QY 841 QASITVSVSGEAWSGYGEYKGTASNYLAELOQEDTITCFISTPQSEFTLPKDPETPLIM 900  
Db 841 QASITVSVSGEAWSGYGEYKGTASNYLAELOQEDTITCFISTPQSEFTLPKDPETPLIM 900  
QY 901 VGPCTGVAPRGVQARKOLKEQGSGLGEAHLYFGCRSPHEDLYQEELNAQSEGIITL 960  
Db 901 VGPCTGVAPRGVQARKOLKEQGSGLGEAHLYFGCRSPHEDLYQEELNAQSEGIITL 960  
QY 961 HTAFSRMPNPKTYVQVHVMDQCKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
Db 961 HTAFSRMPNPKTYVQVHVMDQCKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
QY 1021 HOVSEADARLWLOLEEKGRYKDVWAG 1048  
Db 1021 HOVSEADARLWLOLEEKGRYKDVWAG 1048

## RESULT 2

TYPE\_BACSU  
ID TYPE\_BACSU STANDARD; PRT; 1054 AA.  
AC O08336;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Probable bifunctional P-450:NADPH-P450 reductase 2 [Includes:  
DE Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase  
DE (EC 1.6.2.4)].  
GN CYPE OR CYP102A3.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=97453479; PubMed=9308178;  
RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,  
RA Duesterhoeft A., Ehrlich S.D.,  
RT "Sequence of the Bacillus subtilis genome region in the vicinity of  
RT the lev operon reveals two new extracytoplasmic function RNA  
RT polymerase sigma factors Sigv and Sigz.";  
RL Microbiology 143:2939-2943(1997).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=98044033; PubMed=9384377;  
RA Kunst F., Ogawara N., Mosser I., Albertini A.M., Alloni G.,  
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Boursier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
RA Chou S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,  
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
RA Fritz C., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
RA Ghim S.G., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,  
RA Guiseppi G., Guy B.J., Haga K., Haech J., Harwood C.R., Henaut A.,  
RA Hilbert H., Hollappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,  
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
RA Priescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
RA Rieger M., Rivoita C., Rocha E., Roche M., Rose M., Sadale I.,  
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,  
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,  
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,  
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;  
RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
RT subtilis".  
RL Nature 390:249-256(1997).  
CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE  
CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME  
CC P450 (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
CC ferrocyclochrome.  
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
CC oxidized flavoprotein + H(2)O.  
CC -1- COFACTOR: FAD AND FMN (BY SIMILARITY).  
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME  
CC P450 FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: U93874; AAB80867.1; -;  
DR EMBL: Z99117; CAB14658.1; -;  
DR HSSP: P14779; 1JPZ.  
DR Subtilist; BG12299; cYPE.  
DR InterPro: IPR001128; Cytochrome\_P450.  
DR InterPro: IPR003097; FAD\_binding.  
DR InterPro: IPR001709; FPN\_cyt\_redctse.  
DR InterPro: IPR001226; Flavodoxin.  
DR InterPro: IPR001433; Oxred\_FAD/NAD(P).  
DR Pfam: PF00067; p450; 1.  
DR Pfam: PF00175; NAD\_binding; 1.  
DR Pfam: PF00258; flavodoxin; 1.  
DR Pfam: PF00667; FAD\_binding; 1.  
DR PRINTS; PR00371; FPNCR.  
DR PRINTS; PR00385; p450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;  
KW Complete proteome.  
FT DOMAIN 1 475 CYTOCHROME P450.  
FT DOMAIN 472 1053 NADPH-P-450 REDUCTASE.  
FT BINDING 403 403 HEME (BY SIMILARITY).  
SQ SEQUENCE 1054 AA; 118675 MW; 705F8E27866C110 CRC64;  
Query Match 2.7%; Score 28; DB 1; Length 1054;

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Best Local Similarity 100.0%; Pred. NO. 9.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 LDDENRYQIITFLIAGHETTSGLLSFA 276
Db 252 LDDENRYQIITFLIAGHETTSGLLSFA 279

RESULT 3
CYPD_BACSU STANDARD; PRT; 1061 AA.
AC 008384;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable bifunctional P-450:NADPH-P450 reductase 1 [Includes:
DE Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
DE (EC 1.6.2.4)].
GN CYPD OR CYP102A2.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97453479; PubMed=93081178;
RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
RA Duesterhoeft A., Ehrlich S.D.;
RT "Sequence of the Bacillus subtilis genome region in the vicinity of
RT the lev operon reveals two new extracytoplasmic function RNA
RT polymerase sigma factors Sigv and Sigz.";
RL Microbiology 143:2939-2943(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Broutillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Chou S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinolis S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Masuda S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogawa K., Ogivara A., Oudega B., Park S.H.,
RA Parro V., Fohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Riegerman E., Pujic C., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
CC P450 (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferrocyclochrome.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +

```

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oxidized flavoprotein + H(2)O.
-1- COFACTOR: FAD AND FMN (By similarity).
-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
P450 FAMILY.
-----
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or send an email to license@isb-sib.ch).
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EMBL; D87979; BAA20123.1; -.
DR EMBL; 299107; CAB12544.1; -.
DR HSSP; F14779; 1JFZ.
DR Subtilist; BG12871; cypD.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001709; FPN_cyt_reductse.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00067; P450; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR Pfam; PF00258; Flavodoxin; 1.
DR Pfam; PF00667; FAD_binding; 1.
DR PRINTS; PR00371; FPNCR.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
KW Complete proteome.
FT DOMAIN 1 474 CYTOCHROME P450.
FT DOMAIN 475 1061 NADPH-P-450 REDUCTASE.
FT BINDING 403 403 HEME (BY SIMILARITY).
SQ SEQUENCE 1061 AA; 119467 MW; 7915DACC20578978 CRC64;

Query Match 2.0%; Score 21; DB 1; Length 1061;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 DMTRLTDLTGLGCFNYRFS 164
Db 146 DMTRLTDLTGLGCFNYRFS 166

RESULT 4
NCPR_SCHPO STANDARD; PRT; 678 AA.
AC P36587; Q9USU6;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
GN CCRI OR SPBC39A10.01 OR SPBC365.17.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93038553; PubMed=1417773;
RA Miles J.S.;
RT "Structurally and functionally conserved regions of cytochrome P-450
RT reductase as targets for DNA amplification by the polymerase chain
RT reaction. Cloning and nucleotide sequence of the Schizosaccharomycetes
RL pombe cDNA.";
RL Biochem. J. 287:195-200(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;

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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moutle S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Voicakert G., Aert R., Robben J., Grymonprez B.,  
RA Welte J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Bartell B.G., Nurse P.,  
RT "The genome sequence of Schizosaccharomyces pombe.";  
RL Nature 415:871-880(2002).  
CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
CC ferrocyclochrome.  
CC -1- COFACTOR: FAD AND FMN.  
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
CC REDUCTASE.  
CC -----  
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CC -----  
DR EMBL: X64702; CAA45956.1; -;  
DR EMBL: AL078627; CAB44769.1; -;  
DR EMBL: AL034463; CAA22429.2; -;  
DR PIR: S29123; S29123.  
DR HSP: P00388; IAMO.  
DR InterPro: IPR003097; FAD\_binding.  
DR InterPro: IPR001094; Flavodoxin\_like.  
DR InterPro: IPR001226; Flavodoxin.  
DR InterPro: IPR001433; Oxred\_FAD/NAD(P).  
DR Pfam: PF001175; NAD\_binding\_1.  
DR Pfam: PF00258; flavodoxin; 1.  
DR Pfam: PF00667; FAD\_binding; 1.  
DR PRINTS: PR00369; FLAVODOXIN.  
KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
KW Transmembrane.  
FT TRANSMEM 7 23 POTENTIAL.  
FT NP\_BIND 153 184 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
FT NP\_BIND 306 317 FAD (ADP PART) (BY SIMILARITY).  
FT NP\_BIND 437 448 FAD (FLAVIN PART) (BY SIMILARITY).  
FT NP\_BIND 535 553 NADP (RIBOSE PART) (BY SIMILARITY).  
FT NP\_BIND 630 646 NADP (ADP PART) (BY SIMILARITY).  
SQ SEQUENCE 678 AA; 76774 MW; 6AEDDFBA6DE39C8F CRC64;

Query Match

1.5%; Score 16; DB 1; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPRGEV 914  
DB 534 IMVPGTGVAPRGEV 549  
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RESULT 5  
NCPR\_HUMAN STANDARD; PRT; 676 AA.  
AC P16435; Q16455; Q9H3M8;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).  
GN POR OR CYPOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RC SEQUENCE.  
RX MEDLINE=90105390; PubMed=2513880;  
RA Haniu M., McManus M.E., Birkett D.J., Lee T.D., Shively J.E.;  
RT "Structural and functional analysis of NADPH-cytochrome P-450  
RT reductase from human liver: complete sequence of human enzyme and  
RL NADPH-binding sites.";  
RL Biochemistry 28:8639-8645(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92198003; PubMed=1550342;  
RA Shephard E.A., Palmer C.N., Segall H.J., Phillips I.R.;  
RT "Quantification of cytochrome P450 reductase gene expression in human  
RT tissues.";  
RL Arch. Biochem. Biophys. 294:168-172(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC Tissue=Liver;  
RA Czerwinski M., Sahni M., Madan A., Parkinson A.;  
RT "Polymorphism of human CYPOR: expression of new allele.";  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Murakami H.O., Ogawa H., Nisimoto Y.;  
RT "cDNA cloning and characterization of NADPH-cytochrome P-450 reductase  
RT in human HL-60 cell.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 61-241.  
RX MEDLINE=99156068; PubMed=10048323;  
RA Zhao Q., Modi S., Smith G., Paine M., McDonagh P.D., Wolf C.R.,  
RA Tew D., Lian L.Y., Roberts G.C., Driessen H.P.;  
RT "Crystal structure of the FMN-binding domain of human cytochrome P450  
RT reductase at 1.93 A resolution.";  
RL Protein Sci. 8:298-306(1999).  
CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
CC ferrocyclochrome.  
CC -1- COFACTOR: FAD AND FMN.  
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
CC REDUCTASE.  
CC -----  
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CC DR EMBL; S90469; AAB21814.1; -
CC DR EMBL; AP258341; AAG09798.1; -
CC DR EMBL; AB051763; BAB18572.1; -
CC DR PIR; A33421; A33421.
CC DR PDB; 1B1C; 24-NOV-99.
CC DR Genew; HGNC:9208; POR.
CC DR MTM; 124015; -
CC DR InterPro; IPR003097; FAD_binding.
CC DR InterPro; IPR001709; FPN_cyt_reductase.
CC DR InterPro; IPR001094; Flavodoxin_like.
CC DR InterPro; IPR001226; Flavodoxin.
CC DR InterPro; IPR001433; Oxred_FAD/NAD(P).
CC DR Pfam; PF00175; NAD_binding; 1.
CC DR Pfam; PF00258; flavodoxin; 1.
CC DR PRINTS; PR00369; FLAVODOXIN.
CC DR PRINTS; PR00371; FPNCR.
CC DR Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
KW Membrane; Acetylation; Polymorphism; 3D-structure.
FT INIT_MET 0
FT MOD_RES 1
FT NP_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 528 546 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 622 638 NADP (ADP PART) (BY SIMILARITY).
FT VARIANT 499 499 A -> V.
FT VARIANT 550 550 R -> Q.
FT CONFLICT 404 404 M -> L (IN REF. 4).
FT CONFLICT 517 517 F -> L (IN REF. 2 AND 4).
FT CONFLICT 536 537 VA -> WH (IN REF. 2).
SQ SEQUENCE 676 AA; 76558 MW; 883EA13797020D70 CRC64;

Query Match 1.1%; Score 12; DB 1; Length 676;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVGPGTGVAPF 910
Db 528 IMVGPGTGVAPF 539
|||||

RESULT 6
NCPR_CAVPO STANDARD; PRT; 677 AA.
AC P37039;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
GN POR.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=Hartley;
RA MEDLINE=93041995; PubMed=1420354;
RX Ohguya S., Goda T., Ishizaki K., Kamataki T., Shinriki N.;
RT "Molecular cloning and sequence analysis of guinea-pig NADPH-
RL cytochrome P-450 oxidoreductase.";
RL Biochim. Biophys. Acta 1171:103-105(1992).
RN [2]
RN ERRATUM.
RX MEDLINE=93385164; PubMed=8373812;
RA Ohguya S., Goda T., Ishizaki K., Kamataki T., Shinriki N.;
RL Biochim. Biophys. Acta 1174:313-313(1993).

-1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
-1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2
ferricytochrome.
-1- COFACTOR: FAD AND FMN.
-1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
REDUCTASE.
-1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO ORIGINATE FROM MOUSE.

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EMBL; D10498; BAA01385.1; -
PIR; S27158; S27158.
HSP; P00388; IAMO.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPN_cyt_reductase.
InterPro; IPR001094; Flavodoxin_like.
InterPro; IPR001226; Flavodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
Membrane; Acetylation.
FT INIT_MET 0
FT MOD_RES 1
FT NP_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 529 547 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 624 640 NADP (ADP PART) (BY SIMILARITY).
SQ SEQUENCE 677 AA; 76650 MW; 4CA758F28EB84938 CRC64;

Query Match 1.1%; Score 12; DB 1; Length 677;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVGPGTGVAPF 910
Db 528 IMVGPGTGVAPF 539
|||||

RESULT 7
NCPR_MOUSE STANDARD; PRT; 677 AA.
AC P37040;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
GN POR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=ddy;
RX MEDLINE=94281246; PubMed=8011664;
RX Ohguya S., Ishizaki K., Kamataki T., Shinriki N.;

```



"Mouse NADPH-cytochrome P-450 oxidoreductase: molecular cloning and functional expression in yeast.";  
 Blochim. Biophys. Acta 1186:137-141(1994).  
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
 TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
 ferricytochrome.  
 CC -1- COFACTOR: FAD AND FMN.  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
 ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
 FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
 NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
 REDUCTASE.  
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 CC -----  
 CC EMBL; D17571; BAA04496.1; -;  
 DR HSSP; P00388; 1A00.  
 DR SWISS-2DPAGE; P37040; MOUSE.  
 DR MGI; MGI:97744; POR.  
 DR InterPro; IPR003097; FAD\_binding.  
 DR InterPro; IPR001709; FPN\_cyt\_redtase.  
 DR InterPro; IPR001094; Flavodoxin\_like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00175; NAD\_binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
 DR Pfam; PF00687; FAD\_binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
 KW Membrane; Acetylation.  
 FT INIT\_MET 0 BY SIMILARITY.  
 FT MOD\_RES 1 1 ACETYLATION (BY SIMILARITY).  
 FT NP\_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).  
 FT NP\_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).  
 FT NP\_BIND 529 547 NADP (RIBOSE PART) (BY SIMILARITY).  
 FT NP\_BIND 624 640 NADP (ADP PART) (BY SIMILARITY).  
 SQ SEQUENCE 677 AA; 76912 MW; 0065C14D0E1C5EF8 CRC64;  
 Query Match 1.18; Score 12; DB 1; Length 677;  
 Best Local Similarity 100.0%; Pred. No. 0.0013;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 899 IMVGPGRGVAPF 910  
 DB 528 IMVGPGRGVAPF 539  
 RESULT 8  
 NCPR\_PIG STANDARD; PRT; 677 AA.  
 AC P04175;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).  
 GN POR.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Amorn J., Preiss B., Stender B., Viale M., Repp R.Z., Lampert F.,  
 RA Kroger M., Lumper L.;  
 RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE.  
 RX MEDLINE-87101085; PubMed-3099837;  
 RA Hanlu M., Iyanagi T., Miller P., Lee T.D., Shively J.E.;  
 RT "Complete amino acid sequence of NADPH-cytochrome P-450 reductase  
 from porcine hepatic microsomes.";  
 RL Biochemistry 25:7906-7911(1986).  
 RN [3]  
 RP SEQUENCE OF 56-677.  
 RX MEDLINE-87075664; PubMed-3098240;  
 RA Vogel F., Lumper L.;  
 RT "Complete structure of the hydrophilic domain in the porcine NADPH-  
 cytochrome P-450 reductase.";  
 RL Biochem. J. 236:871-878(1986).  
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
 TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
 ferricytochrome.  
 CC -1- COFACTOR: FAD AND FMN.  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
 ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
 FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
 NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
 REDUCTASE.  
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 CC -----  
 CC EMBL; L33893; AAA85368.1; -;  
 DR PIR; A00403; RDPG04.  
 DR PIR; A25584; A25584.  
 DR HSSP; P16435; IB1C.  
 DR InterPro; IPR003097; FAD\_binding.  
 DR InterPro; IPR001709; FPN\_cyt\_redtase.  
 DR InterPro; IPR001094; Flavodoxin\_like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00175; NAD\_binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
 DR Pfam; PF00687; FAD\_binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
 KW Membrane; Acetylation.  
 FT INIT\_MET 0 0  
 FT MOD\_RES 1 1  
 FT NP\_BIND 169 200 ACETYLATION (BY SIMILARITY).  
 FT NP\_BIND 313 324 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 450 460 FAD (ADP PART) (BY SIMILARITY).  
 FT NP\_BIND 528 546 FAD (FLAVIN PART) (BY SIMILARITY).  
 FT NP\_BIND 623 639 NADP (RIBOSE PART) (BY SIMILARITY).  
 FT NP\_BIND 639 674 NADP (ADP PART) (BY SIMILARITY).  
 FT CONFLICT 54 54 S -> T (IN REF. 2).  
 FT CONFLICT 163 163 T -> S (IN REF. 2).  
 FT CONFLICT 174 174 N -> D (IN REF. 3).  
 FT CONFLICT 339 339 T -> A (IN REF. 3).  
 FT CONFLICT 378 378 N -> D (IN REF. 3).  
 FT CONFLICT 400 400 Q -> E (IN REF. 3).  
 FT CONFLICT 446 446 R -> L (IN REF. 2).  
 FT CONFLICT 502 502 N -> D (IN REF. 3).  
 FT CONFLICT 508 508 V -> L (IN REF. 2 AND 3).  
 FT CONFLICT 674 674 D -> N (IN REF. 3).  
 SQ SEQUENCE 677 AA; 76701 MW; 26073A0B97EE3DFF CRC64;

Query Match 1.1%; Score 12; DB 1; Length 677;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPF 910  
Db 528 IMVPGTGVAPF 539

RESULT 9

NCPR-RABIT STANDARD; PRT; 679 AA.

ID NCPR-RABIT STANDARD; PRT; 679 AA.

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).

GN POR.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=87137361; PubMed=3029050;

RA Katagiri M., Murakami H., Yabusaki Y., Sugiyama T., Okamoto M.,

RA Yamano T., Ohkawa H.;

RT "Molecular cloning and sequence analysis of full-length cDNA for

RT rabbit liver NADPH-cytochrome P-450 reductase mRNA.";

RL J. Biochem. 100:945-954(1986).

RN [2]

RP PARTIAL SEQUENCE OF 1-81.

RC TISSUE=Liver;

RX MEDLINE=82167456; PubMed=6802823;

RA Black S.D., Coon M.J.;

RT "Structural features of liver microsomal NADPH-cytochrome P-450

RT reductase. Hydrophobic domain, hydrophilic domain, and connecting

RT region.";

RL J. Biol. Chem. 257:5929-5938(1982).

CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP

CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON

CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.

CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2

CC ferrocycytochrome.

CC -1- COFACTOR: FAD AND FMN.

CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE

CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.

CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL

CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN

CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE

CC REDUCTASE.

CC -----

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CC -----

DR EMBL; D00101; BAA00063.1; -

DR EMBL; X04610; CAA28279.1; -

DR PIR; A25505; A25505.

DR PIR; A05233; A05233.

DR HSSP; P16435; LBIC.

DR InterPro; IPR003097; FAD\_binding.

DR InterPro; IPR001709; FPN\_cyt\_redtse.

DR InterPro; IPR001094; Flavodoxin\_like.

DR InterPro; IPR001226; Flavodoxin.

DR InterPro; IPR001433; Oxred\_FAD/NAD(P).

DR Pfam; PF00175; NAD\_binding.1.

DR Pfam; PF00258; flavodoxin; 1.

DR Pfam; PF00667; FAD\_binding.1.

DR PRINTS; PR00369; FLAVODOXIN.

DR PRINTS; PR00371; FPNCR.

KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;

KW Membrane; Acetylation.

FT MOD\_RES 72 72 ACETYLATION.

FT NP\_BIND 171 202 FMN (PYRIMIDINE PART) (BY SIMILARITY).

FT NP\_BIND 315 326 FAD (ADP PART) (BY SIMILARITY).

FT NP\_BIND 452 462 FAD (FLAVIN PART) (BY SIMILARITY).

FT NP\_BIND 530 548 NADP (RIBOSE PART) (BY SIMILARITY).

FT NP\_BIND 625 641 NADP (ADP PART) (BY SIMILARITY).

FT CONFLICT 40 41 YW -> NY (IN REF. 2).

FT CONFLICT 53 53 E -> N (IN REF. 2).

SQ SEQUENCE 679 AA; 76588 MW; B1A163FA53A5988B CRC64;

Query Match 1.1%; Score 12; DB 1; Length 679;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPF 910

Db 530 IMVPGTGVAPF 541

RESULT 10

NCPR-YEAST STANDARD; PRT; 690 AA.

ID NCPR-YEAST STANDARD; PRT; 690 AA.

AC P16603;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).

GN NCPL OR NCPR1 OR PRD1 OR YHR042W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A. AND SEQUENCE OF 1-12 AND 44-61.

RX MEDLINE=89008184; PubMed=3139648;

RA Yabusaki Y., Murakami H., Ohkawa H.;

RT "Primary structure of Saccharomyces cerevisiae NADPH-cytochrome P450

RT reductase deduced from nucleotide sequence of its cloned gene.";

RL J. Biochem. 103:1004-1010(1988).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C / AB972;

RX MEDLINE=94378003; PubMed=8091229;

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,

RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,

RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,

RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,

RA Nham M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,

RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,

RA Vaudin M.;

RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome

RT VIII.";

RL Science 265:2077-2082(1994).

CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP

CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON

CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.

CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2

CC ferrocycytochrome.

CC -1- COFACTOR: FAD AND FMN.

CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE

CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.

CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL

CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN

CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE

CC REDUCTASE.

CC -----

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CC EMBL; D13788; BAA02936.1; -.
CC EMBL; U00062; AAB68904.1; -.
CC PIR; A41447; A41447.
CC PIR; A46735; A46735.
CC HSSP; P00388; IAMO.
CC SGB; S0001084; NCPI.
CC InterPro; IPR003097; FAD_binding.
CC InterPro; IPR001709; FPN_cyt_redctse.
CC InterPro; IPR001094; Flavodoxin_like.
CC InterPro; IPR001226; Flavodoxin.
CC InterPro; IPR001433; Oxred_FAD/NAD(P).
CC Pfam; PF00175; NAD_binding; 1.
CC Pfam; PF00258; flavodoxin; 1.
CC Pfam; PF00667; FAD_binding; 1.
CC PRINTS; PR00369; FLAVODOXIN.
CC PRINTS; PR00371; FPNCR.
CC Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
KW Membrane.
FT INIT_MET 0 0
FT NP_BIND 148 179 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 300 311 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 435 445 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 536 554 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 638 654 NADP (ADP PART) (BY SIMILARITY).
FT VARIANT 473 473 V -> G.
FT CONFLICT 422 422 T -> N (IN REF. 1).
SQ SEQUENCE 690 AA; 76640 MW; FEFA18F6AB2BBD5 CRC64;
```

Query Match 1.1%; Score 12; DB 1; Length 690;

Best Local Similarity 100.0%; Pred. No. 0.0013; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 902 GPGTGVPFRGF 913
Db 539 GPGTGVPFRGF 550
|||||
```

RESULT 11

```
ID NCPR_PHAU STANDARD; PRT; 690 AA.
AC P37116;
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
OS Phaseolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucrosts 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3916;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=cv Berken; TISSUE=Seedling;
RX MEDLINE=93219390; PubMed=8464904;
RA Shet M.S., Sathasivan K., Arlotto M.A., Mehdy M.C., Estabrook R.W.;
RT "Purification, characterization, and cDNA cloning of an NADPH-
cytochrome P450 reductase from mung bean.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2890-2894(1993).
CC -!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
TO CYTOCHROME P450.
CC -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
ferricytochrome.
CC -!- COFACTOR: FAD AND FMN.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE
ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
CC -!- PTM: GLYCOSYLATED.
CC -!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
```

FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE REDUCTASE.

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```
CC EMBL; L07843; AAA34240.1; -.
CC HSSP; P00388; IAMO.
CC InterPro; IPR003097; FAD_binding.
CC InterPro; IPR001709; FPN_cyt_redctse.
CC InterPro; IPR001094; Flavodoxin_like.
CC InterPro; IPR001226; Flavodoxin.
CC InterPro; IPR001433; Oxred_FAD/NAD(P).
CC Pfam; PF00175; NAD_binding; 1.
CC Pfam; PF00258; flavodoxin; 1.
CC Pfam; PF00667; FAD_binding; 1.
CC PRINTS; PR00369; FLAVODOXIN.
CC PRINTS; PR00371; FPNCR.
CC Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
KW Membrane; Glycoprotein.
FT NP_BIND 179 210 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 325 336 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 465 475 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 544 562 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 639 654 NADP (ADP PART) (BY SIMILARITY).
FT CARBOHYD 275 275 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 690 AA; 76506 MW; 592966167E8561DE CRC64;
```

Query Match 1.0%; Score 11; DB 1; Length 690;

Best Local Similarity 100.0%; Pred. No. 0.014; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 826 PRYYSISSSPR 836
Db 467 PRYYSISSSPR 477
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RESULT 12

```
ID YB63_SCHPO STANDARD; PRT; 571 AA.
AC Q09744;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C12C2.03c in chromosome II.
GN SPBC12C2.03C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
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RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
 RA Welteijns I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Sapakowski G.V., Ussery D., Barrell B.G., Nurse P.,  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880(2002).  
 CC -1- SIMILARITY: SOME, TO NADPH-CYTOCHROME P450 REDUCTASES.  
 CC -----  
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 CC -----

DR EMBL; Z54140; CAA90816.1;  
 DR InterPro: IPR003097; FAD\_binding.  
 DR InterPro: IPR001433; Oxid\_FAD/NAD(P).  
 DR Pfam: PF001175; NAD\_binding; 1.  
 DR Pfam: PF00667; FAD\_binding; 1.  
 KW Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.  
 SQ SEQUENCE 571 AA; 6396 MW; D2EE992789307249 CRC64;

Query Match 1.0%; Score 10; DB 1; Length 571;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 906 GVAPFRGFVQ 915  
 DB 405 GVAPFRGFVQ 414  
 |||||

## RESULT 13

NCPR\_SALTR NCPR\_SALTR STANDARD; PRT; 601 AA.  
 AC P19618;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R)  
 DE (fragments).  
 OS Salmo trutta (Brown trout).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 OX NCBI\_TaxID=8032;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=88008061; PubMed=3116019;  
 RA Urenjak J., Linder D., Lumper L.;  
 RT "Structural comparison between the trout and mammalian hydrophilic  
 RT domain of NADPH-cytochrome P-450 reductase.";  
 RL J. Chromatogr. A 397:123-136(1987).  
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
 CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
 CC ferrocycytochrome.  
 CC -1- COFACTOR: FAD AND FMN.  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN

CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
 CC REDUCTASE.  
 DR PIR: A28577; A28577.  
 DR HSSP: P16435; 1B1C.  
 DR InterPro: IPR001709; FPN\_cyt\_redctase.  
 DR InterPro: IPR001094; Flavodoxin\_like.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
 KW Membrane.  
 FT NON\_TER 1  
 FT NON\_CONS 426 427  
 FT NON\_CONS 434 435  
 SQ SEQUENCE 601 AA; 68304 MW; BC801767DEID44C9 CRC64;

Query Match 1.0%; Score 10; DB 1; Length 601;

Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 941 EDYLYQEELE 950  
 DB 494 EDYLYQEELE 503  
 |||||

## RESULT 14

NCPR\_MOUSE NCPR\_MOUSE STANDARD; PRT; 1429 AA.  
 ID Q92034; Q64208;  
 AC 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Nitric-oxide synthase, brain (EC 1.14.13.39) (NOS, type I) (Neuronal  
 DE NOS) (N-NOS) (nNOS) (Constitutive NOS) (NC-NOS) (bNOS).  
 GN NOS1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS N-NOS-1 AND N-NOS-2).  
 RC STRAIN-BALB/C; TISSUE=Brain;  
 RX MEDLINE=93312283; PubMed=7686743;  
 RA Ogura T., Yokoyama T., Fujisawa H., Kurashima Y., Esumi H.;  
 RT "Structural diversity of neuronal nitric oxide synthase mRNA in the nervous  
 RT system.";  
 RL Biochem. Biophys. Res. Commun. 193:1014-1022(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM NNOS MU).  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=96212184; PubMed=8626668;  
 RA Silvagno F., Xia H., Bredt D.S.;  
 RT "Neuronal nitric-oxide synthase-mu, an alternatively spliced isoform  
 RT expressed in differentiated skeletal muscle.";  
 RL J. Biol. Chem. 271:11204-11208(1996).  
 RN [3]  
 RP ALTERNATIVE SPLICING (ISOFORMS NNOS BETA; NNOS GAMMA AND NNOS MU).  
 RX MEDLINE=97351924; PubMed=9208206;  
 RA Brenman J.E., Xia H., Chao D.S., Black S.M., Bredt D.S.;  
 RT "Regulation of neuronal nitric oxide synthase through alternative  
 RT transcripts.";  
 RL Dev. Neurosci. 19:224-231(1997).  
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND  
 CC PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A  
 CC NEUROTRANSMITTER. ISOFORM NNOS MU MAY BE AN EFFECTOR ENZYME FOR  
 CC THE DYSTROPHIN COMPLEX.  
 CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +  
 CC nitric oxide + N NADP(+).  
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 CC THE ENZYME (BY SIMILARITY).  
 CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN. INHIBITED BY  
 CC N-NOS-INHIBITING PROTEIN (PIN) WHICH MAY PREVENT THE DIMERIZATION

OF THE PROTEIN (BY SIMILARITY).  
 -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 -1- SUBCELLULAR LOCATION: IN SKELETAL MUSCLE, NNOS IS LOCALIZED BENEATH THE SARCOLEMA OF FAST-TWITCH MUSCLE FIBER BY ASSOCIATING WITH THE DYSTROPHIN GLYCOPROTEIN COMPLEX.  
 -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; N-NOS-1 (SHOWN HERE), N-NOS-2, NNOS BETA, NNOS GAMMA AND NNOS MU/MUSCLE-SPECIFIC; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE NERVOUS SYSTEM; EXPRESSED IN CEREBRUM, OLFACTORY BULB, HIPPOCAMPUS, MIDBRAIN, CEREBELLUM, PONS, MEDULLA OBLONGATA, AND SPINAL CORD. ALSO FOUND IN SKELETAL MUSCLE, WHERE IT IS LOCALIZED BENEATH THE SARCOLEMA OF FAST TWITCH MUSCLE FIBERS, AND IN SPLEEN, HEART, KIDNEY, AND LIVER. N-NOS-1 AND N-NOS-2 ARE FOUND IN ALL PARTS OF THE NERVOUS SYSTEM. NNOS BETA AND GAMMA OCCUR IN A REGION-SPECIFIC MANNER IN THE BRAIN AND NNOS BETA EXPRESSION IS DEVELOPMENTALLY REGULATED. NNOS MU IS ONLY FOUND IN MATURE SKELETAL AND CARDIAC MUSCLES.  
 -1- INDUCTION: BY CHOLINERGIC AGONISTS ACTING AT INOSITOL PHOSPHATE-LINKED MUSCARINIC RECEPTORS IN CARDIAC MYOCYTES.  
 -1- DOMAIN: THE PDZ DOMAIN IN THE N-TERMINAL PART OF THE NEURONAL ISOFORM PARTICIPATES IN PROTEIN-PROTEIN INTERACTION, AND IS RESPONSIBLE FOR TARGETING NNOS TO SYNAPTIC MEMBRANES IN MUSCLES.  
 -1- DISEASE: IN MDX MICE (MOUSE MODEL OF DYSTROPHINOPATHY) THE DYSTROPHIN COMPLEX IS DISRUPTED AND NNOS IS DISPLACED FROM SARCOLEMA AND ACCUMULATES IN THE CYTOSOL.  
 -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 -1- SIMILARITY: CONTAINS 1 PDZ/DRH DOMAIN.  
 -----  
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 EMBL: D14552; BAA03415.1; -;  
 DR EMBL: S81982; AAB36469.1; -;  
 DR HSSP: P29476; 1P20.  
 DR MGD: MGI:97360; Nos1.  
 DR InterPro: IPR003097; FAD\_binding.  
 DR InterPro: IPR001709; FPN\_Cyt\_redctse.  
 DR InterPro: IPR001094; Flavodoxin\_like.  
 DR InterPro: IPR001226; Flavodoxin.  
 DR InterPro: IPR004030; NO\_synthase.  
 DR InterPro: IPR001433; Oxred\_FAD/NAD(P).  
 DR InterPro: IPR001478; PDZ.  
 DR Pfam: PF00175; NAD\_binding; 1.  
 DR Pfam: PF00258; flavodoxin; 1.  
 DR Pfam: PF00595; PDZ; 1.  
 DR Pfam: PF00667; FAD\_binding; 1.  
 DR Pfam: PF02898; NO\_synthase; 1.  
 DR PRINTS: PR00369; FLAVODOXIN.  
 DR PRINTS: PR00371; PFNCR.  
 DR SMART: SM00228; PDZ; 1.  
 DR PROSITE: PS60001; NOS; 1.  
 DR PROSITE: PS0106; PDZ; 1.  
 DR Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;  
 KW Alternative splicing; Multigene family.  
 FT DOMAIN 17 99  
 FT DOMAIN 163 240  
 FT NNOS-INHIBITING PROTEIN (PIN)-BINDING (BY  
 FT SIMILARITY).  
 FT BINDING 415  
 FT HEME (BY SIMILARITY).  
 FT CALMODULIN-BINDING (POTENTIAL).  
 FT NP\_BIND 725 745  
 FT FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 881 912  
 FT FAD (ADP PART) (BY SIMILARITY).  
 FT NP\_BIND 1027 1038  
 FT FAD (FLAVIN PART) (BY SIMILARITY).  
 FT NP\_BIND 1170 1180  
 FT NADP (RIBOSE PART) (BY SIMILARITY).  
 FT NP\_BIND 1245 1263  
 FT NADP (ADP PART) (BY SIMILARITY).  
 FT NP\_BIND 1343 1358  
 FT MISSING (IN ISOFORM NNOS BETA).  
 FT MISSING (IN ISOFORM NNOS BETA).  
 FT TGLQVD -> WRGLGS (IN ISOFORM NNOS BETA).  
 FT VARSPLIC 231 236  
 FT MISSING (IN ISOFORM NNOS GAMMA).  
 FT VARSPLIC 1 331  
 FT MISSING (IN ISOFORM N-NOS-2).  
 FT VARSPLIC 504 608

FT VARSPLIC 839 839 K -> KYPEPLRFFPRKGPSLSHVDSSEAHSLVAARDSQHR  
 FT (IN ISOFORM NNOS MU).  
 SQ SEQUENCE 1429 AA; 160472 MW; 3782848D65B41BFC CRC64;  
 Query Match 1.0%; Score 10; DB 1; Length 1429;  
 Best Local Similarity 100.0%; Pred. No. 0.27;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 826 PRYSISSSP 835  
 Db 1172 PRYSISSSP 1181  
 RESULT 15  
 NOS1\_RAT STANDARD; PRT; 1429 AA.  
 ID NOS1\_RAT  
 AC P29476; P70594;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Nitric-oxide synthase, brain (EC 1.14.13.39) (NOS, type I) (Neuronal NOS) (N-NOS) (NNOS) (Constitutive NOS) (NC-NOS) (BNOS).  
 GN NOS1 OR BNOS.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE-Brain;  
 RX MEDLINE=91287795; PubMed=1712077;  
 RA Bredt D.S., Hwang P.M., Glatt C.L., Lowenstein C., Reed R.R., Snyder S.H.;  
 RT "Cloned and expressed nitric oxide synthase structurally resembles cytochrome P-450 reductase.";  
 RL Nature 351:714-718(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM PNNOS).  
 RC STRAIN-Fischer 344; TISSUE-Penis;  
 RX MEDLINE=96400229; PubMed=8806605;  
 RA Magee T., Fuentes A.M., Garban H., Rajavashisth T., Marquez D., Rodriguez J.A., Rajfer J., Gonzalez-Cadavid N.F.;  
 RT "Cloning of a novel neuronal nitric oxide synthase expressed in penis and lower urinary tract.";  
 RL Biochem. Biophys. Res. Commun. 226:145-151(1996).  
 RN [3]  
 RP MUTAGENESIS OF TYR-588.  
 RX MEDLINE=21134290; PubMed=11237702;  
 RA Sato Y., Sagami I., Matsui T., Shimizu T.;  
 RT "Unusual role of Tyr588 of neuronal nitric oxide synthase in controlling substrate specificity and electron transfer.";  
 RL Biochem. Biophys. Res. Commun. 281:621-626(2001).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.25 ANGSTROMS) OF 14-125.  
 RX MEDLINE=99238815; PubMed=10221915;  
 RA Hallier B.J., Christopherson K.S., Prehoda K.E., Bredt D.S., Lim W.A.;  
 RT "Unexpected modes of PDZ domain scaffolding revealed by structure of nNOS-synrophin complex.";  
 RL Science 284:812-815(1999).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 963-1397.  
 RX MEDLINE=21463055; PubMed=11473123;  
 RA Zhang J., Martasek P., Paschke R., Shea T., Masters B.S.S., Kim J.-J.P.;  
 RT "Crystal structure of the FAD/NADPH-binding domain of rat neuronal nitric-oxide synthase. Comparisons with nadph-cytochrome p450 oxidoreductase.";  
 RL J. Biol. Chem. 276:37506-37513(2001).  
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A NEUROTRANSMITTER.  
 CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +

nitric oxide + N NADP(+).  
-1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
CC CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
CC CC THE ENZYME (BY SIMILARITY).  
CC CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN. INHIBITED BY  
CC CC N-NOS-INHIBITING PROTEIN (PIN) WHICH MAY PREVENT THE DIMERIZATION  
CC CC OF THE PROTEIN (BY SIMILARITY).  
CC CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC CC -1- SUBCELLULAR LOCATION: IN SKELETAL MUSCLE. NNOS IS LOCALIZED  
CC CC BENEATH THE SARCOLEMA OF FAST-TWITCH MUSCLE FIBER BY ASSOCIATING  
CC CC WITH THE DYSTROPHIN GLYCOPROTEIN COMPLEX (BY SIMILARITY).  
CC CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; N-NOS-1 (SHOWN HERE), N-NOS-2  
CC CC AND PNNOS; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC CC -1- TISSUE SPECIFICITY: ISOFORM N-NOS1 IS EXPRESSED IN BRAIN. ISOFORM  
CC CC PNNOS IS EXPRESSED IN THE PENIS, URETHRA, PROSTATE, AND SKELETAL  
CC CC MUSCLE, AND COEXIST WITH THE CEREBELLAR NNOS IN THE PELVIC  
CC CC PLEXUS, BLADDER AND LIVER, AND IS DETECTABLE IN THE CEREBELLUM.  
CC CC -1- DOMAIN: THE PDZ DOMAIN IN THE N-TERMINAL PART OF THE NEURONAL  
CC CC ISOFORM PARTICIPATES IN PROTEIN-PROTEIN INTERACTION, AND IS  
CC CC RESPONSIBLE FOR TARGETING NNOS TO SYNAPTIC MEMBRANES IN MUSCLES  
CC CC (BY SIMILARITY).  
CC CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
CC CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.  
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CC CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR DR EMBL; X59949; CAA42574.1; -  
DR DR EMBL; U67309; AAC52782.1; -  
DR DR PIR; S16233; S16233  
DR DR PDB; 1QAU; 06-MAR-00.  
DR DR PDB; 1QAV; 06-MAR-00.  
DR DR PDB; 1F20; 10-OCT-01.  
DR DR InterPro: IPR003097; FAD\_binding.  
DR DR InterPro: IPR001709; FPN\_cyt\_redctse.  
DR DR InterPro: IPR001094; Flavodoxin\_like.  
DR DR InterPro: IPR001226; Flavodoxin.  
DR DR InterPro: IPR004030; NO\_synthase.  
DR DR InterPro: IPR001433; Oxred\_FAD/NAD(P).  
DR DR InterPro: IPR001478; PDZ.  
DR DR Pfam; PF00175; NAD\_binding; 1.  
DR DR Pfam; PF00258; flavodoxin; 1.  
DR DR Pfam; PF00395; PDZ; 1.  
DR DR Pfam; PF00667; FAD\_binding; 1.  
DR DR Pfam; PF02898; NO\_synthase; 1.  
DR DR PRINTS; PR00369; FLAVODOXIN.  
DR DR PRINTS; PR00371; FPNCR.  
DR DR SMART; SM00228; PDZ; 1.  
DR DR PROSITE; PS60001; NOS; 1.  
DR DR PROSITE; PS50106; PDZ; 1.  
DR DR Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;  
KW KW Alternative splicing; Multigene family; 3D-structure.  
FT FT DOMAIN 17 99 PDZ.  
FT FT DOMAIN 163 240 NNOS-INHIBITING PROTEIN (PIN)-BINDING (BY  
FT FT SIMILARITY).  
FT FT BINDING 415 415 HEME (BY SIMILARITY).  
FT FT BINDING 588 588 CARBOXYLATE OF THE SUBSTRATE.  
FT FT DOMAIN 725 745 CALMODULIN-BINDING (POTENTIAL).  
FT FT NP\_BIND 881 912 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
FT FT NP\_BIND 1027 1038 FAD (ADP PART) (BY SIMILARITY).  
FT FT NP\_BIND 1170 1180 FAD (FLAVIN PART) (BY SIMILARITY).  
FT FT NP\_BIND 1245 1263 NADP (RIBOSE PART) (BY SIMILARITY).  
FT FT NP\_BIND 1343 1358 NADP (ADP PART) (BY SIMILARITY).  
FT FT VARSPLIC 504 608 MISSING (IN ISOFORM N-NOS-2).  
FT FT VARSPLIC 839 839 K -> KYPEPLRFFPKGPSLSHVDSEAHSLVAARDSQHR  
FT FT (IN ISOFORM PNNOS).  
FT FT MUTAGEN 588 588 Y->H: 50% DECREASE OF ACTIVITY.  
FT FT MUTAGEN 588 588 Y->S: 30% DECREASE OF ACTIVITY.

FT MUTAGEN 588 588 Y->F: NO DECREASE IN ACTIVITY.  
FT CONFLICT 269 269 I -> V (IN REF. 2).  
FT CONFLICT 953 953 P -> A (IN REF. 2).  
FT CONFLICT 1008 1008 F -> S (IN REF. 2).  
FT CONFLICT 1311 1311 A -> V (IN REF. 2).  
SQ SEQUENCE 1429 AA; 160559 MW; 7255C5AE165200F5 CRC64;  
Query Match 1.0%; Score 10; DB 1; Length 1429;  
Best Local Similarity 100.0%; Pred.No. 0.27; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0;  
QY 826 PRYSSSSSP 835  
DB 1172 PRYSSSSSP 1181  
Search completed: May 29, 2003, 08:42:08  
Job time : 27 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:31:47 ; Search time 74 Seconds

(without alignments)

1887.117 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 1048

Sequence: 1 TIKEMPQPTFGELKNPLLL.....RLWLQLEEKGRYAKDVGWAG 1048

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1048	100.0	1048	22	AAB31978 Amino acid sequenc
2	1048	100.0	1048	22	B. megaterium cyto
3	1048	100.0	1048	22	B. megaterium cyto
4	1048	100.0	1049	21	AAY93566 Amino acid sequenc
5	1048	100.0	1049	22	AAB31882 Amino acid sequenc
6	961	91.7	1048	22	AAB31979 Amino acid sequenc
7	860	82.1	1048	22	AAB31980 Amino acid sequenc
8	860	82.1	1048	22	AAB31981 Amino acid sequenc
9	846	80.7	1049	22	AAY72208 Bacillus megateriu
10	266	25.4	1085	12	AA11604 P450 17-alpha/P450

11	17	1.6	17	20	AAV27545	B. megaterium p-45
12	15	1.4	693	16	AAR66738	Cytochrome-P450-ox
13	13	1.2	597	22	AAB49682	Human reductase am
14	13	1.2	700	22	AAY33673	B. bassiana pops r
15	12	1.1	677	22	AAB73901	Human derived cyto
16	12	1.1	677	22	AAB73902	Human derived cyto
17	12	1.1	678	23	ABB57261	Mouse ischaemic co
18	12	1.1	679	8	AAP70546	Sequence of rabbit
19	12	1.1	680	22	AAU27786	Human full-length
20	12	1.1	682	22	AAB82516	Rabbit NADH cytoch
21	12	1.1	685	22	AAU27958	Human contig poly
22	12	1.1	691	11	AAR05234	Sequence of yeast
23	12	1.1	1169	16	AAB76544	Mitochondrial cyto
24	10	1.0	582	22	ABB68450	Drosophila melanog
25	10	1.0	588	23	AAB20656	Helianthus tuberos
26	10	1.0	588	23	AAE16392	Helianthus tuberos
27	10	1.0	628	22	AAG82875	S. epidermidis ope
28	10	1.0	629	23	ABP39549	Staphylococcus epi
29	10	1.0	683	20	AAW85682	Poppy cytochrome p
30	10	1.0	883	20	AAW85680	Poppy cytochrome p
31	10	1.0	1429	14	AA844489	Sequence of all or
32	10	1.0	1430	19	AAW56786	Rat neuronal nitri
33	10	1.0	1430	20	AAW28475	Rat neuronal nitri
34	10	1.0	1433	16	AAR77362	Neuronal nitrogen
35	10	1.0	1433	22	AAB31725	Amino acid sequenc
36	10	1.0	1433	22	AAB66725	Human nitric oxide
37	10	1.0	1463	18	AAW35566	Rat penile neurona
38	10	1.0	1554	20	AAW28476	Human neuronal nit
39	9	0.9	516	22	ABB58868	Drosophila melanog
40	9	0.9	516	23	AAW76367	Drosophila melanog
41	9	0.9	679	21	AAW90596	Candida tropicalis
42	9	0.9	679	21	AAW90597	Candida tropicalis
43	9	0.9	679	22	ABB64462	Drosophila melanog
44	9	0.9	679	23	ABB77082	Candida tropicalis
45	9	0.9	679	23	ABB77083	Candida tropicalis

#### ALIGNMENTS

RESULT 1

AAB31978  
ID AAB31978 standard; Protein: 1048 AA.

XX AC AAB31978;

XX DT 15-MAY-2001 (first entry)

XX DE Amino acid sequence of a Bacillus P450 monooxygenase protein.

XX KW Cytochrome P450 monooxygenase; oxidization; indole; indigo; indorubicin.

XX OS Bacillus megaterium.

XX PN WO200107630-A1.

XX PD 01-FEB-2001.

XX PF 27-JUL-2000; 2000WO-EP07253.

XX PR 27-JUL-1999; 99DE-1035115.

XX PR 18-NOV-1999; 99DE-1055605.

XX PR 22-MAR-2000; 2000DE-1014085.

XX XX (BADI ) BASF AG.

XX PA Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;

XX PI Li Q;

XX XX WPI; 2001-182800/18.

XX DR N-PSDB; AAF54832.

XX PT Cytochrome P450 monooxygenase for oxidizing organic compounds, useful

especially for converting indole to indigo, has wide substrate range -  
 Claim 3; Page 35-39; 54pp; German.  
 The present sequence represents a cytochrome P450 monooxygenase. The  
 specification describes a modified cytochrome P450 monooxygenase which  
 can oxidize at least one of the following types of substrates:  
 CC optionally substituted mono- or poly-cyclic aromatic heterocyclics  
 CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or  
 CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or  
 CC optionally substituted cycloalkanes or cycloalkenes. The modified  
 CC cytochrome P450 monooxygenase are specifically used to oxidize indole  
 CC to indigo and indorubicin. However, they may be used to oxidize many  
 CC other substrates.  
 XX  
 SQ Sequence 1048 AA;

Query Match 100.0%; Score 1048; DB 22; Length 1048;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMQPKTFGELKMLPLNTDKPVQALMKIADLGEIFKFEAPGRVTRYLSSORLIKE 60  
 DB 1 TIKEMQPKTFGELKMLPLNTDKPVQALMKIADLGEIFKFEAPGRVTRYLSSORLIKE 60  
 QY 61 ACDESFRDNLSQLAFVRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAMKGYHAMV 120  
 DB 61 ACDESFRDNLSQLAFVRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAMKGYHAMV 120  
 QY 121 DIAVQLVQWERLNADHEIEVPEDMTLRLLDTGLCGFNRYRNSFYRDPHFITSWRA 180  
 DB 121 DIAVQLVQWERLNADHEIEVPEDMTLRLLDTGLCGFNRYRNSFYRDPHFITSWRA 180  
 QY 181 LDEAMNKLQRANPDDPAYDENKQFQEDIKVMDLVKIIADKASGEOSDILLTHMLNG 240  
 DB 181 LDEAMNKLQRANPDDPAYDENKQFQEDIKVMDLVKIIADKASGEOSDILLTHMLNG 240  
 QY 241 KDPETGEPLDDENIRYQIIITFLAGHETTSGLLSFALYFLVNPHYLQKAAEAAARVLD 300  
 DB 241 KDPETGEPLDDENIRYQIIITFLAGHETTSGLLSFALYFLVNPHYLQKAAEAAARVLD 300  
 QY 301 PVPYSQVQKLVGVNLEALRLWTPAFSLYAKEDVVLGGEYPLEKGDMLVLPOL 360  
 DB 301 PVPYSQVQKLVGVNLEALRLWTPAFSLYAKEDVVLGGEYPLEKGDMLVLPOL 360  
 QY 361 HRDRTIWDVDEFRPERFENSAIPQAFKPFNGQORACIGQOFALHEATLVLGMLKH 420  
 DB 361 HRDRTIWDVDEFRPERFENSAIPQAFKPFNGQORACIGQOFALHEATLVLGMLKH 420  
 QY 421 FPEDEHTNVELDITKLTLPKGEFVVVYKAKSKKIPGLGIPSPSTQSAKKVRKKAENHNT 480  
 DB 421 FPEDEHTNVELDITKLTLPKGEFVVVYKAKSKKIPGLGIPSPSTQSAKKVRKKAENHNT 480  
 QY 481 PLLVLVYSGNMGTAEGTARLADIANSGKFAPOVATLDSHAGNLPREGAVLIVTASNGHP 540  
 DB 481 PLLVLVYSGNMGTAEGTARLADIANSGKFAPOVATLDSHAGNLPREGAVLIVTASNGHP 540  
 QY 541 PNAKQFVDWLQASADEKGVYRVSVFGCGDKNWTYYOKVPAFIDETLAAKGAENIADR 600  
 DB 541 PNAKQFVDWLQASADEKGVYRVSVFGCGDKNWTYYOKVPAFIDETLAAKGAENIADR 600  
 QY 601 GEADASDDPEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPKAMHG 660  
 DB 601 GEADASDDPEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPKAMHG 660  
 QY 661 AFSTNVVASKELQOQPSARSTRHLELELPKEASYQEGDLHGVIPRNYEGIVNRVTFARFGL 720  
 DB 661 AFSTNVVASKELQOQPSARSTRHLELELPKEASYQEGDLHGVIPRNYEGIVNRVTFARFGL 720  
 QY 721 DASQQLRLAEAEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAAKTVCPPHKVEL 780  
 DB 721 DASQQLRLAEAEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAAKTVCPPHKVEL 780

QY 781 EALLEKQAYKEQVLAKRLTMELELLEKYPACEMKFSEFIALLPSIRPRYYSISSPRVDEK 840  
 DB 781 EALLEKQAYKEQVLAKRLTMELELLEKYPACEMKFSEFIALLPSIRPRYYSISSPRVDEK 840  
 QY 841 QASITVSVVSGAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900  
 DB 841 QASITVSVVSGAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900  
 QY 901 VGPGTGVAFRGFVQARKOLKEGOSIGLGAHLYFGCRSPHEDYLYOELENAQSEGIITL 960  
 DB 901 VGPGTGVAFRGFVQARKOLKEGOSIGLGAHLYFGCRSPHEDYLYOELENAQSEGIITL 960  
 QY 961 HTAFSRMPNQPTYYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 DB 961 HTAFSRMPNQPTYYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 QY 1021 HOVSEADARLWLOLEEKGRYAKDVWAG 1048  
 DB 1021 HOVSEADARLWLOLEEKGRYAKDVWAG 1048

RESULT 2  
 AAB46855  
 ID AAB46855 standard; Protein; 1048 AA.  
 XX  
 AC AAB46855;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE B. megaterium cytochrome P450 monooxygenase BM-3 protein.  
 XX  
 KW Cytochrome P450 monooxygenase; BM-3; electron donor system; bioreactor;  
 KW electron transfer; hydroxylatable fatty acid; fatty acid-monoxygenase.  
 OS Bacillus megaterium.  
 XX  
 PN WO200107573-A1.  
 PD  
 PD 01-FEB-2001.  
 PF 27-JUL-2000; 2000WO-EP07251.  
 XX  
 PR 27-JUL-1999; 99DE-1035115.  
 PR 10-MAR-2000; 2000DE-1011723.  
 XX  
 PA (BADI ) BASF AG.  
 XX  
 PI Hauer B., Schmid RD, Schwaneberg U;  
 XX  
 DR WPI; 2001-159709/16.  
 DR N-PSDB; AAF26268.  
 XX  
 PT Novel electron donor system useful for the production of  
 PT omega-hydroxylated fatty acids comprises an inorganic electron sink and  
 PT a mediator which enables the electron transfer -  
 PS Claim 13b; Page 83-86; 94pp; German.  
 XX  
 CC This invention describes a novel electron donor system (M1) that  
 CC transfers electrons to an enzyme with redox properties comprising an  
 CC inorganic, not electrode-bound, electron sink and a mediator which enable  
 CC the electron transfer. The invention also describes (1) transferring (M2)  
 CC oxygen to a hydrocarbon containing hydrogen donor molecule, where the  
 CC hydrogen donor molecule is in a reaction medium comprising the oxygen  
 CC transferring enzyme and (M1) in the presence of oxygen and incubating  
 CC under suitable reaction conditions; (2) the enzymatic production (M3) of  
 CC terminally or subterminally hydroxylated (position omega-1 to omega-4)  
 CC fatty acids comprising: (i) mixing a hydroxylatable fatty acid or fatty  
 CC acid derivative in the presence of (M1) and cytochrome P450  
 CC monooxygenase; and (ii) isolating the hydroxylated product; (3) a  
 CC bioreactor useful for the production of omega-hydroxylated fatty acids as  
 CC described in (2); and (4) detecting (M4) fatty acid-monoxygenases  
 CC comprising: (1) contacting the analyte with a omega-hydroxylatable fatty



CC acid or a derivative comprising a terminal chromophore or fluorescent  
 CC label in (M1); and (ii) qualitatively or quantitatively detecting the  
 CC signal. The invention is useful for the production of omega-hydroxylated  
 CC fatty acids and the detection of fatty acid monooxygenases. The  
 CC invention provides an alternative electron donor system of enzymes with  
 CC redox properties that is cheaper and more efficient, where the enzyme  
 CC comprises cytochrome 450.  
 XX  
 SQ Sequence 1048 AA;

Query Match 100.0%; Score 1048; DB 22; Length 1048;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGLKPLNLTNDKPVQALMTADELGEIKFPEAGRVTRYLSSQRLIKE 60  
 DB 1 TIKEMPOKTFGLKPLNLTNDKPVQALMTADELGEIKFPEAGRVTRYLSSQRLIKE 60  
 QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNMKKAHNILLPSFSQAMKGYHAMV 120  
 DB 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNMKKAHNILLPSFSQAMKGYHAMV 120  
 QY 121 DIAVQLVQWERLNADEHIEVDPEDTRLTLDITGLCGFNFRNSFYRDQPHPPITSMVRA 180  
 DB 121 DIAVQLVQWERLNADEHIEVDPEDTRLTLDITGLCGFNFRNSFYRDQPHPPITSMVRA 180  
 QY 181 LDEAMNKLORANPDDPAYDENKFOEDIKVMDLVDKITADKASGEQSDLLTHMLNG 240  
 DB 181 LDEAMNKLORANPDDPAYDENKFOEDIKVMDLVDKITADKASGEQSDLLTHMLNG 240  
 QY 241 KOPETGEPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPNHVLQKAAEAAARVLVD 300  
 DB 241 KOPETGEPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPNHVLQKAAEAAARVLVD 300  
 QY 301 PVPYSQVQKLVGVNLEALRLMPTAPAFSLYAKEDVVLGGEYPLEKGDMLVLIPO 360  
 DB 301 PVPYSQVQKLVGVNLEALRLMPTAPAFSLYAKEDVVLGGEYPLEKGDMLVLIPO 360  
 QY 361 HRDKTITWDDVEFRERENPNSAIPQAFKPGNGQRACIGQOFALHEATLVGLMWLKH 420  
 DB 361 HRDKTITWDDVEFRERENPNSAIPQAFKPGNGQRACIGQOFALHEATLVGLMWLKH 420  
 QY 421 FDFEDHTNYELDIKETLTLLKPEGVVYKAKSKKIPGLGIPSPSTEQSAKVRKAENAHNT 480  
 DB 421 FDFEDHTNYELDIKETLTLLKPEGVVYKAKSKKIPGLGIPSPSTEQSAKVRKAENAHNT 480  
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 DB 481 PLLVLYGSGNMTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 540  
 QY 541 PNAKQFVWLQDQASADEKGVRYSVFGCGDKNWTYOKVPAFIDETLAAKGAENIADR 600  
 DB 541 PNAKQFVWLQDQASADEKGVRYSVFGCGDKNWTYOKVPAFIDETLAAKGAENIADR 600  
 QY 601 GEADSDDEFTGYEWEHREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 660  
 DB 601 GEADSDDEFTGYEWEHREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 660  
 QY 661 AFSTNVVASKELQOQPSASRTHLELPEKASQYQGDHGLGVIPRYNGVIVNRTARFGL 720  
 DB 661 AFSTNVVASKELQOQPSASRTHLELPEKASQYQGDHGLGVIPRYNGVIVNRTARFGL 720  
 QY 721 DASQQIRLAEAEKLAHLPLAKTVSVYELLOVYVELODPVTRTOLRAMAAKTVCPPHKVEL 780  
 DB 721 DASQQIRLAEAEKLAHLPLAKTVSVYELLOVYVELODPVTRTOLRAMAAKTVCPPHKVEL 780  
 QY 781 EALLERQAYKEQVLAKRLTLMLELLERYPACEMKFSFIALPSIRPRYISISSPRVDEK 840  
 DB 781 EALLERQAYKEQVLAKRLTLMLELLERYPACEMKFSFIALPSIRPRYISISSPRVDEK 840  
 QY 841 QASITVSVSGEAWSGYGEYKGTASNYLAELOEGDITTCFISTPQSEFTLPKDPETPLIM 900  
 DB 841 QASITVSVSGEAWSGYGEYKGTASNYLAELOEGDITTCFISTPQSEFTLPKDPETPLIM 900

QY 901 VPGTGVAPFRGFVQARKOLKEQGSIGLGAHLYFGCRSPHEDYLYOELENAOSEGIITL 960  
 DB 901 VPGTGVAPFRGFVQARKOLKEQGSIGLGAHLYFGCRSPHEDYLYOELENAOSEGIITL 960  
 QY 961 HTAFSRMPNQPRTYVQHVMEQDGKLLIQLDQGAHFYICGDSQMAPAVATLKMYSADV 1020  
 DB 961 HTAFSRMPNQPRTYVQHVMEQDGKLLIQLDQGAHFYICGDSQMAPAVATLKMYSADV 1020  
 QY 1021 HQVSEADARLWLOOLEEKGRYAKDVWAG 1048  
 DB 1021 HQVSEADARLWLOOLEEKGRYAKDVWAG 1048

RESULT 3  
 AAB46856  
 ID AAB46856 standard; Protein; 1048 AA.  
 XX  
 AC AAB46856;  
 AC  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE B. megaterium cytochrome P450 monooxygenase BM-3 protein.  
 XX  
 KW Cytochrome P450 monooxygenase; BM-3; site-specific mutagenesis;  
 KW aliphatic carboxylic acid hydroxylation; fatty acid.  
 OS Bacillus megaterium.  
 XX  
 PN W0200107574-A2.  
 XX  
 PD 01-FEB-2001.  
 XX  
 PF 27-JUL-2000; 2000WO-EP07252.  
 XX  
 PR 27-JUL-1999; 99DE-1035115.  
 PR 10-MAR-2000; 2000DE-1011723.  
 XX  
 PA (BADI ) BASF AG.  
 XX  
 PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;  
 PI Li Q;  
 XX  
 WPI: 2001-159710/16.  
 N-PSDB; AAF26324.  
 XX  
 PT New modified cytochrome P450 mono-oxygenase, useful for producing  
 PT hydroxylated aliphatic carboxylic acids and derivatives, has altered  
 PT substrate specificity -  
 XX  
 PS Claim 3; Page 41-45; 49pp; German.  
 XX  
 CC This invention describes a novel modified cytochrome P450 (I) having, as  
 CC a result of site-specific mutagenesis of its substrate-binding domain,  
 CC an altered substrate profile, relative to the wild-type, when used for  
 CC terminal and/or subterminal enzymatic hydroxylation of aliphatic  
 CC carboxylic acids. The invention also describes (1) nucleic acid (II)  
 CC encoding (I), and its complement; (2) expression cassette (EC) containing  
 CC (II) and control elements; (3) a vector containing at least one EC; (4)  
 CC recombinant microorganisms transformed with at least one vector of (3);  
 CC and (5) enzymatic production of terminally and/or subterminally  
 CC hydroxylated aliphatic carboxylic acids (A) using the microorganisms of  
 CC (4), or isolated (I). (I), and recombinant cells that express them, are  
 CC used to produce hydroxylated aliphatic carboxylic acids or their  
 CC derivatives (esters and amides). (I) have altered substrate specificity,  
 CC especially for hydroxylation of 8-12C fatty acids at the omega-1, -2  
 CC and/or -3 positions, and may also have increased reactivity and/or  
 CC regioselectivity.  
 XX  
 SQ Sequence 1048 AA;

Query Match 100.0%; Score 1048; DB 22; Length 1048;  
 Best Local Similarity 100.0%; Pred. No. 0;

		Matches 1048;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	TIKEMPQKTFGELKPLNLTNDKPVQALMKIADLGEIFKFEAPGRVTRYLSSORLIKE	60							
Db	1	TIKEMPQKTFGELKPLNLTNDKPVQALMKIADLGEIFKFEAPGRVTRYLSSORLIKE	60							
QY	61	ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	120							
Db	61	ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	120							
QY	121	DIAVQLVQKWERLNADHEIETVEDMTRLTDLTIGLCGFNYRNSFYRDPHPFITSMVRA	180							
Db	121	DIAVQLVQKWERLNADHEIETVEDMTRLTDLTIGLCGFNYRNSFYRDPHPFITSMVRA	180							
QY	181	LDEAMNKLORANPDPAIDENKROQEDIKVNDLVDKIADRKASGEOSDILLFHLNG	240							
Db	181	LDEAMNKLORANPDPAIDENKROQEDIKVNDLVDKIADRKASGEOSDILLFHLNG	240							
QY	241	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYELVKNPHVLQKAAEAAARVLVD	300							
Db	241	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYELVKNPHVLQKAAEAAARVLVD	300							
QY	301	PVPSYKQVKQLKYVGMVNLNEALRLMPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPOL	360							
Db	301	PVPSYKQVKQLKYVGMVNLNEALRLMPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPOL	360							
QY	361	HRDKTIWGDVVEEFPERFENSAIPQHAFFKFGNGORACIGQOFALHEATLVGLMKLKH	420							
Db	361	HRDKTIWGDVVEEFPERFENSAIPQHAFFKFGNGORACIGQOFALHEATLVGLMKLKH	420							
QY	421	FPEDHTNYELDIKETLTLKPGFVVKAKSKIPILGGIPSPSTEQSAKKVKKKAENAHNT	480							
Db	421	FPEDHTNYELDIKETLTLKPGFVVKAKSKIPILGGIPSPSTEQSAKKVKKKAENAHNT	480							
QY	481	PLLVLYGSNMGTAEGTARDLADIAKSGFAPQVATLDHSHAGNLPREGAVLIIVTASNGHP	540							
Db	481	PLLVLYGSNMGTAEGTARDLADIAKSGFAPQVATLDHSHAGNLPREGAVLIIVTASNGHP	540							
QY	541	PDNAKQFVMDLQASADEVKGVYRVFGCGDKNWTATYQKVPFIDETLAAGAENIADR	600							
Db	541	PDNAKQFVMDLQASADEVKGVYRVFGCGDKNWTATYQKVPFIDETLAAGAENIADR	600							
QY	601	GEADASDDPEGTYEWEHREHMWDVAAYFNLDITENSEDNKSTLSLQFVDSAADMLAKMHG	660							
Db	601	GEADASDDPEGTYEWEHREHMWDVAAYFNLDITENSEDNKSTLSLQFVDSAADMLAKMHG	660							
QY	661	AFSTNVASKELOQPGSARSTRHLELPKEASYOEGDHLGVIIPRYEGIVNRVTARFGL	720							
Db	661	AFSTNVASKELOQPGSARSTRHLELPKEASYOEGDHLGVIIPRYEGIVNRVTARFGL	720							
QY	721	DASQIIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL	780							
Db	721	DASQIIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL	780							
QY	781	EALLKEQAYKEOVLAKRUTMLLEKYPACEMKFSEFIALPSIRPRYSISSSPRVDEK	840							
Db	781	EALLKEQAYKEOVLAKRUTMLLEKYPACEMKFSEFIALPSIRPRYSISSSPRVDEK	840							
QY	841	QASITVSVVSGEAWSGYEGYKIGIASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIM	900							
Db	841	QASITVSVVSGEAWSGYEGYKIGIASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIM	900							
QY	901	VGPFGTVAPFRGFGVQARQKLEQOSGLGEAHLFCGRSPHEDYLYQEELENAQSGIITL	960							
Db	901	VGPFGTVAPFRGFGVQARQKLEQOSGLGEAHLFCGRSPHEDYLYQEELENAQSGIITL	960							
QY	961	HTAFSRMPNQPTYVQHVNQDQKKLIELLDQGAHFYICGGDSQMAVAEATLMKSYADV	1020							
Db	961	HTAFSRMPNQPTYVQHVNQDQKKLIELLDQGAHFYICGGDSQMAVAEATLMKSYADV	1020							
QY	1021	HOVSADARLWQLQLEEKGRYAKDVWAG	1048							
Db	1021	HOVSADARLWQLQLEEKGRYAKDVWAG	1048							

RESULT 4

AA93566

ID AAY93566 standard; Protein; 1049 AA.

XX AAY93566;

XX AC

XX 25-SEP-2000 (first entry)

XX DE

XX Amino acid sequence of the P450-BM3 sequence.

XX KW

XX Terpene; cycloalkene; haem-containing enzyme; mutant; oxidation;

XX KW

XX infection; P450-BM3.

XX OS

XX Unidentified.

XX FH

XX Key

XX Misc-difference 303

XX FT

XX /note= "Val encoded by GCT"

XX FT

XX Misc-difference 471

XX FT

XX /note= "Val encoded by GCA"

XX WO200031273-A2.

XX PN

XX 02-JUN-2000.

XX PD

XX 19-NOV-1999; 99WO-GB03873.

XX PF

XX 19-NOV-1998; 98GB-0025421.

XX PR

XX (ISIS-) ISIS INNOVATION LTD.

XX PA

XX Wong LL, Bell SG, Carmichael AB;

XX PI

XX WPI; 2000-451679/39.

XX DR

XX N-PSDB; AAA46648.

XX PT

XX Process for oxidizing acyclic or cyclic terpenes, cycloalkenes, or

XX PT

XX derivatives for preventing or treating infection in human or animal

XX PT

XX body comprises mutant haem-containing enzyme which has substitution of

XX PT

XX amino acid in the active site -

XX PS

XX Disclosure; Page 51-53; 63pp; English.

XX CC

XX The specification describes a process for oxidizing an acyclic or

XX CC

XX cyclic terpene, a cycloalkene, or a derivative. The process comprises

XX CC

XX oxidizing the compound with a mutant haem-containing enzyme which

XX CC

XX comprises a substitution of an amino acid in the active site by an

XX CC

XX amino acid with a less polar side-chain. The process is useful for

XX CC

XX oxidizing an acyclic or cyclic terpene, a cycloalkene, or their

XX CC

XX derivatives. The process is also useful for producing an oxidation

XX CC

XX product useful for preventing or treating infection in a human or

XX CC

XX animal body. The present sequence represents the amino acid sequence of

XX CC

XX the P450-BM3 sequence. The protein is used to construct enzymes

XX CC

XX for use in the process of the invention.

XX SQ

XX Sequence 1049 AA;

XX Query Match

XX 100.0%; Score 1048; DB 21; Length 1049;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPQKTFGELKPLNLTNDKPVQALMKIADLGEIFKFEAPGRVTRYLSSORLIKE 60

Db 2 TIKEMPQKTFGELKPLNLTNDKPVQALMKIADLGEIFKFEAPGRVTRYLSSORLIKE 61

QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 120

Db 62 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 121

QY 121 DIAVQLVQKWERLNADHEIETVEDMTRLTDLTIGLCGFNYRNSFYRDPHPFITSMVRA 180

Db 121 DIAVQLVQKWERLNADHEIETVEDMTRLTDLTIGLCGFNYRNSFYRDPHPFITSMVRA 180

Db 122 DIAVLQVKWERLNADHEIEVPEDMTLRLDTLGLGCFNYRNSFYRDQPHPTTSMVRA 181  
QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVWMDLVDKTIADRKASGEQSDLLTHMLNG 240  
Db 182 LDEAMNKLQANPDDPAYDENKRFQEDIKVWMDLVDKTIADRKASGEQSDLLTHMLNG 241  
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVQLKAAEEAARVLD 300  
Db 242 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVQLKAAEEAARVLD 301  
QY 301 PVPSTKQVKQLKYGVMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLPOL 360  
Db 302 PVPSTKQVKQLKYGVMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLPOL 361  
QY 361 HRDKTIWGDVVEEFRPERFENPSAIPQHAFKPFNGQORACIGQOFALHEATLVGLMMLKH 420  
Db 362 HRDKTIWGDVVEEFRPERFENPSAIPQHAFKPFNGQORACIGQOFALHEATLVGLMMLKH 421  
QY 421 FPFEDHTNYELDIKETLTLLKPEGFFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 480  
Db 422 FPFEDHTNYELDIKETLTLLKPEGFFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 481  
QY 481 PLLVLYGSNMGTAEFTARDLADIAKSGFAPQVATLDSHAGNLPRBGAVLIIVTASNGHP 540  
Db 482 PLLVLYGSNMGTAEFTARDLADIAKSGFAPQVATLDSHAGNLPRBGAVLIIVTASNGHP 541  
QY 541 PDNAKQFVMDLQASADEVKGVYRVSFVGGCKDNWATTYOKVPAFIDETLAAGAENIADR 600  
Db 542 PDNAKQFVMDLQASADEVKGVYRVSFVGGCKDNWATTYOKVPAFIDETLAAGAENIADR 601  
QY 601 GEADASDDPEGTYEWEHREHWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 660  
Db 602 GEADASDDPEGTYEWEHREHWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 661  
QY 661 AFSTNVVASKELQQPGSABSTHLELPELPEKASYQEGDHLGYIPRNYEGIVNRVTAARFGL 720  
Db 662 AFSTNVVASKELQQPGSABSTHLELPELPEKASYQEGDHLGYIPRNYEGIVNRVTAARFGL 721  
QY 721 DASQQIRLEAEKEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAAKTVCPPHKVEL 780  
Db 722 DASQQIRLEAEKEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAAKTVCPPHKVEL 781  
QY 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKSEFIALPSIRPRYYSISSSPRVDEK 840  
Db 782 EALLEKQAYKEQVLAKRLTMELEKYPACEMKSEFIALPSIRPRYYSISSSPRVDEK 841  
QY 841 QASITVSVYSGEAWSGYGVKGTASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900  
Db 842 QASITVSVYSGEAWSGYGVKGTASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 901  
QY 901 VGPGTGVPFRGFVQARKQKQGGQSLGSAHLYFGCRSPHEDYLYQEELENAQSEGIITL 960  
Db 902 VGPGTGVPFRGFVQARKQKQGGQSLGSAHLYFGCRSPHEDYLYQEELENAQSEGIITL 961  
QY 961 HTAFSRMPNQPTTYVQHVMEQDGKLLIELLDQGAHYICGDSQMAPAVEATLMKSYADV 1020  
Db 962 HTAFSRMPNQPTTYVQHVMEQDGKLLIELLDQGAHYICGDSQMAPAVEATLMKSYADV 1021  
QY 1021 HQVSEADARLWLQOLEEKGRYAKDVWAG 1048  
Db 1022 HQVSEADARLWLQOLEEKGRYAKDVWAG 1049

RESULT 5

AAB31882

ID AAB31882 standard; Protein; 1049 AA.

XX AAB31882;

AC AAB31882;

XX 15-MAY-2001 (first entry)

DT 15-MAY-2001 (first entry)

XX 15-MAY-2001 (first entry)

DE Amino acid sequence of a Bacillus P450 monooxygenase protein.

XX Amino acid sequence of a Bacillus P450 monooxygenase protein.

KW Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.  
XX Bacillus megaterium.  
XX WO200107630-A1.  
PN 01-FEB-2001.  
XX 27-JUL-2000; 2000WO-EP07253.  
PF 27-JUL-1999; 99DE-1035115.  
XX 18-NOV-1999; 99DE-1055605.  
PR 22-MAR-2000; 2000DE-1014085.  
XX (BADI ) BASF AG.  
PA Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;  
XX Li Q;  
PI WPI; 2001-182800/18.  
DR Cytochrome P450 monooxygenase for oxidizing organic compounds, useful  
XX especially for converting indole to indigo, has wide substrate range -  
PT Disclosure; Page 41-44; 54pp; German.  
PS The present sequence represents a cytochrome P450 monooxygenase. The  
XX specification describes a modified cytochrome P450 monooxygenase which  
CC can oxidize at least one of the following types of substrates:  
CC optionally substituted mono- or poly-cyclic aromatic heterocycles  
CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or  
CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or  
CC optionally substituted cycloalkanes or cycloalkenes. The modified  
CC cytochrome P450 monooxygenase are specifically used to oxidize indole  
CC to indigo and indorubicin. However, they may be used to oxidise many  
CC other substrates.  
XX

Sequence 1049 AA;

Query Match 100.0%; Score 1048; DB 22; Length 1049;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPQKTFGELKNLPLNTDKPVQALMKIADDELGEIFKEFAPGRVTRYLSSQRLIKE 60  
Db 2 TIKEMPQKTFGELKNLPLNTDKPVQALMKIADDELGEIFKEFAPGRVTRYLSSQRLIKE 61  
QY 61 ACDESFRDKNLSQALKFVRDPAFGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 120  
Db 62 ACDESFRDKNLSQALKFVRDPAFGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 121  
QY 121 DIAVLQVKWERLNADHEIEVPEDMTLRLDTLGLGCFNYRNSFYRDQPHPTTSMVRA 180  
Db 122 DIAVLQVKWERLNADHEIEVPEDMTLRLDTLGLGCFNYRNSFYRDQPHPTTSMVRA 181  
QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVWMDLVDKTIADRKASGEQSDLLTHMLNG 240  
Db 182 LDEAMNKLQANPDDPAYDENKRFQEDIKVWMDLVDKTIADRKASGEQSDLLTHMLNG 241  
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVQLKAAEEAARVLD 300  
Db 242 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVQLKAAEEAARVLD 301  
QY 301 PVPSTKQVKQLKYGVMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLPOL 360  
Db 302 PVPSTKQVKQLKYGVMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLPOL 361  
QY 361 HRDKTIWGDVVEEFRPERFENPSAIPQHAFKPFNGQORACIGQOFALHEATLVGLMMLKH 420  
Db 362 HRDKTIWGDVVEEFRPERFENPSAIPQHAFKPFNGQORACIGQOFALHEATLVGLMMLKH 421  
QY 421 FPFEDHTNYELDIKETLTLLKPEGFFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 480  
XX FPFEDHTNYELDIKETLTLLKPEGFFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 480

Db 422 DFDHNTNYELDKETLTLPKPGFVVKAKSKKIPGLGIPSPSTEQSAKKVRKAENAHNT 481  
 QY 481 PLLVLGSGNMGTAETGARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 540  
 Db 482 PLLVLGSGNMGTAETGARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 541  
 QY 541 PDNAKQFVDWLQDQASADEVKGVYRVFGCGDKNWTATYQKVPFIDETLAAGAENIADR 600  
 Db 542 PDNAKQFVDWLQDQASADEVKGVYRVFGCGDKNWTATYQKVPFIDETLAAGAENIADR 601  
 QY 601 GADASDDPEGTYEWEHMHWSDAVAAYFNLDIENSEDNKSTLSLQFVDSADMPAKMHG 660  
 Db 602 GADASDDPEGTYEWEHMHWSDAVAAYFNLDIENSEDNKSTLSLQFVDSADMPAKMHG 661  
 QY 661 AFSTNVASKELQQPGSARSTRHLELPEKASVQEGDHLGVIIPRYGIVNRVTARGL 720  
 Db 662 AFSTNVASKELQQPGSARSTRHLELPEKASVQEGDHLGVIIPRYGIVNRVTARGL 721  
 QY 721 DASQOIRLEAEERKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTCPPHKVEL 780  
 Db 722 DASQOIRLEAEERKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTCPPHKVEL 781  
 QY 781 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFEFTALLPSIRPRIYSSSSPRVDEK 840  
 Db 782 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFEFTALLPSIRPRIYSSSSPRVDEK 841  
 QY 841 QASITVSVSGAWSGYGEYKGIASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIM 900  
 Db 842 QASITVSVSGAWSGYGEYKGIASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIM 901  
 QY 901 VGPFGTVAPFRGFGVQARKQKQSGSLGEAHLVFCRSPHEDYLYQEELENAQSGEITL 960  
 Db 902 VGPFGTVAPFRGFGVQARKQKQSGSLGEAHLVFCRSPHEDYLYQEELENAQSGEITL 961  
 QY 961 HTAFSRMPNPQTYVQHVMEQDQKLLIELLDQGAHFYICGDSQMAVAPAEATLMKSYADV 1020  
 Db 962 HTAFSRMPNPQTYVQHVMEQDQKLLIELLDQGAHFYICGDSQMAVAPAEATLMKSYADV 1021  
 QY 1021 HOVSADARLWLQLEEKGRYAKDVWAG 1048  
 Db 1022 HOVSADARLWLQLEEKGRYAKDVWAG 1049

RESULT 6  
 AAB31979  
 ID AAB31979 standard; Protein; 1048 AA.  
 XX  
 AC AAB31979;  
 XX  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Amino acid sequence of a modified P450 monooxygenase protein.  
 XX  
 KW Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.  
 XX  
 OS Bacillus megaterium.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 87  
 FT /note= "wild type Phe changed to Val"  
 XX  
 PN WO200107630-A1.  
 XX  
 PD 01-FEB-2001.  
 XX  
 PF 27-JUL-2000; 2000WO-EP07253.  
 XX  
 PR 27-JUL-1999; 99DE-1035115.  
 PR 18-NOV-1999; 99DE-1055605.  
 PR 22-MAR-2000; 2000DE-1014085.  
 XX  
 PA (BADI ) BASF AG.  
 XX

PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;  
 PI Li Q;  
 XX  
 DR WPI; 2001-182800/18.  
 XX  
 PT Cytochrome P450 monooxygenase for oxidizing organic compounds, useful  
 PT especially for converting indole to indigo, has wide substrate range -  
 XX  
 PS Claim 5; Page -; 54pp; German.  
 XX  
 CC The present sequence represents a modified cytochrome P450 monooxygenase.  
 CC The specification describes a modified cytochrome P450 monooxygenase  
 CC which can oxidize at least one of the following types of substrates:  
 CC optionally substituted mono- or poly-cyclic aromatic heterocyclics  
 CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or  
 CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or  
 CC optionally substituted cycloalkanes or cycloalkenes. The modified  
 CC cytochrome P450 monooxygenase are specifically used to oxidize indole  
 CC to indigo and indorubicin. However, they may be used to oxidise many  
 CC other substrates.  
 CC note: this sequence does not appear in the specification; it was created  
 CC using information provided.  
 XX  
 SQ Sequence 1048 AA;  
 Query Match 91.7%; Score 961; DB 22; Length 1048;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 961; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 88 TSWTEKNWKAHNLLPSFSQQAAMGYHAMVMDIAVLQVKWERLNADHEIEVEDMTR 147  
 Db 88 TSWTEKNWKAHNLLPSFSQQAAMGYHAMVMDIAVLQVKWERLNADHEIEVEDMTR 147  
 QY 148 LTLDITIGLCGNYRNSFYRDPHPFITSMVRALDEAMNKLRANPDPAIDENKRFQE 207  
 Db 148 LTLDITIGLCGNYRNSFYRDPHPFITSMVRALDEAMNKLRANPDPAIDENKRFQE 207  
 QY 208 DIKVMNDLVDKIIADRKASGSDLLTHMLNGKDPETGEPLDDENIRYQITITFLIAGHE 267  
 Db 208 DIKVMNDLVDKIIADRKASGSDLLTHMLNGKDPETGEPLDDENIRYQITITFLIAGHE 267  
 QY 268 TTSGLLSFALYFLVKNPHVLOKAEAAARLVDPVPSYKQVKQKLYGMVNEALRLMPT 327  
 Db 268 TTSGLLSFALYFLVKNPHVLOKAEAAARLVDPVPSYKQVKQKLYGMVNEALRLMPT 327  
 QY 328 APFSLYAKEDTVLGGEYPLEKDELMVLIPQLHRDKTIWGDVVEEPRFENFSAIPQ 387  
 Db 328 APFSLYAKEDTVLGGEYPLEKDELMVLIPQLHRDKTIWGDVVEEPRFENFSAIPQ 387  
 QY 388 HAFKPFNGQACIGQQFALHEATLVLCMLKHFDFEDHTNYELDIKETLTLPKPGFVVK 447  
 Db 388 HAFKPFNGQACIGQQFALHEATLVLCMLKHFDFEDHTNYELDIKETLTLPKPGFVVK 447  
 QY 448 AKSKKIPGLGIPSPSTEQSAKKVRKAENAHNTPLLVLYSGNMGTAETGARDLADIAKSK 507  
 Db 448 AKSKKIPGLGIPSPSTEQSAKKVRKAENAHNTPLLVLYSGNMGTAETGARDLADIAKSK 507  
 QY 508 GFAPQVATLDSHAGNLPREGAVLIIVTASNGHPNPAKQFVDWLQDQASADEVKGVYRV 567  
 Db 508 GFAPQVATLDSHAGNLPREGAVLIIVTASNGHPNPAKQFVDWLQDQASADEVKGVYRV 567  
 QY 568 CGGDKNWTATYQKVPFIDETLAAGAENIADRGEADASDDFEGTYEWEHMHWSDAVAAY 627  
 Db 568 CGGDKNWTATYQKVPFIDETLAAGAENIADRGEADASDDFEGTYEWEHMHWSDAVAAY 627  
 QY 628 FNLDIENSEDNKSTLSLQFVDSADMPAKMHGAFSTNVVASKELQQPGSARSTRHLEIE 687  
 Db 628 FNLDIENSEDNKSTLSLQFVDSADMPAKMHGAFSTNVVASKELQQPGSARSTRHLEIE 687  
 QY 688 LPKEASVQEGDHLGVIIPRYGIVNRVTARGLDASQOIRLEAEERKLAHLPLAKTVSVE 747  
 Db 688 LPKEASVQEGDHLGVIIPRYGIVNRVTARGLDASQOIRLEAEERKLAHLPLAKTVSVE 747

748 ELQYVELQDPVTRTQLRAMAATVCPHPKVELEALLEKQAYKEQVLAKRLTLMLELEKY 807  
 748 ELQYVELQDPVTRTQLRAMAATVCPHPKVELEALLEKQAYKEQVLAKRLTLMLELEKY 807  
 808 PACEMKFSFIALPSPRIRPRYSISSPRVDEKQASITVSVSGEAWSGYGEYKGIASNY 867  
 808 PACEMKFSFIALPSPRIRPRYSISSPRVDEKQASITVSVSGEAWSGYGEYKGIASNY 867  
 868 LAELQEGDITTCFISIPQSEFTLPKDPETPLIMVPGTGVAAPRGFQVARKQLKEQGSL 927  
 868 LAELQEGDITTCFISIPQSEFTLPKDPETPLIMVPGTGVAAPRGFQVARKQLKEQGSL 927  
 928 GEALYFGCRSPHEDLYOELENAQSEGIITLHTAFSRMPNPKTYVQHVMEQDGKKLI 987  
 928 GEALYFGCRSPHEDLYOELENAQSEGIITLHTAFSRMPNPKTYVQHVMEQDGKKLI 987  
 988 ELDDOGAHHFYICGDSQMAPAVEATLMKSYADHVQVSEADARLWLOOLEEKGRYAKDVWA 1047  
 988 ELDDOGAHHFYICGDSQMAPAVEATLMKSYADHVQVSEADARLWLOOLEEKGRYAKDVWA 1047  
 1048 G 1048  
 1048 G 1048  
 RESULT 7  
 AAB31980  
 ID AAB31980 standard; Protein; 1048 AA.  
 AC AAB31980;  
 XX  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Amino acid sequence of a modified P450 monooxygenase protein.  
 XX  
 KW Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.  
 XX  
 OS Bacillus megaterium.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 87  
 FT Misc-difference /note= "wild type Phe changed to Val"  
 FT Misc-difference 188  
 FT Misc-difference /note= "wild type Leu changed to Gln"  
 XX  
 PN W0200107630-A1.  
 XX  
 PD 01-FEB-2001.  
 XX  
 PF 27-JUL-2000; 2000WO-EP07253.  
 XX  
 PR 27-JUL-1999; 99DE-1035115.  
 PR 18-NOV-1999; 99DE-1055605.  
 PR 22-MAR-2000; 2000DE-1014085.  
 XX  
 PA (BADI ) BASF AG.  
 XX  
 PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;  
 PI Li Q;  
 XX  
 DR WPI; 2001-182800/18.  
 XX  
 XX Cytochrome P450 monooxygenase for oxidizing organic compounds, useful  
 XX especially for converting indole to indigo, has wide substrate range -  
 PT  
 PT  
 XX Claim 5; Page -: 54pp; German.  
 PS  
 XX The present sequence represents a modified cytochrome P450 monooxygenase.  
 CC The specification describes a modified cytochrome P450 monooxygenase  
 CC which can oxidize at least one of the following types of substrates:  
 CC optionally substituted mono- or poly-cyclic aromatic heterocyclics  
 CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or  
 CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or

CC optionally substituted cycloalkanes or cycloalkenes. The modified  
 CC cytochrome P450 monooxygenase are specifically used to oxidize indole  
 CC to indigo and indorubicin. However, they may be used to oxidise many  
 CC other substrates.  
 CC note: this sequence does not appear in the specification; it was created  
 CC using information provided.  
 XX  
 SQ Sequence 1048 AA;  
 Query Match 82.1%; Score 860; DB 22; Length 1048;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 189 QRANPDPPAYDENKRFQEDIKVANDLVKIIADRKASGEQSDLLTHMLNGKDPETGEP 248  
 DB 189 QRANPDPPAYDENKRFQEDIKVANDLVKIIADRKASGEQSDLLTHMLNGKDPETGEP 248  
 QY 249 LDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVDPVPSYKQV 308  
 DB 249 LDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVDPVPSYKQV 308  
 QY 309 KQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQLHRDKTIWG 368  
 DB 309 KQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQLHRDKTIWG 368  
 QY 369 DDVEEFPERFENPSAIPQAHAFKPFNGQACIQQFALHEATVLCGMLKHDFEDHTN 428  
 DB 369 DDVEEFPERFENPSAIPQAHAFKPFNGQACIQQFALHEATVLCGMLKHDFEDHTN 428  
 QY 429 YELDIKETLTKPEGFVVKAKSKKIPGLGIPSPSTEQSAKKVRKKAENAHNTPLLVLGYS 488  
 DB 429 YELDIKETLTKPEGFVVKAKSKKIPGLGIPSPSTEQSAKKVRKKAENAHNTPLLVLGYS 488  
 QY 489 NMCTAECTARDLADIAAMSKGFAPQVATLDSHAGNLPREGAVLIVTASVNGHPPDNKQFV 548  
 DB 489 NMCTAECTARDLADIAAMSKGFAPQVATLDSHAGNLPREGAVLIVTASVNGHPPDNKQFV 548  
 QY 549 DWLDOASADEVKGVYSVFCGDKNWTATYQKPAFIDETLAAGAENIADRGADASDD 608  
 DB 549 DWLDOASADEVKGVYSVFCGDKNWTATYQKPAFIDETLAAGAENIADRGADASDD 608  
 QY 609 FEGTYEWEHMHMSDVAAAYFNLOIENSEDNKSTLSLQFVDSAADMPLAKHGAFTNWVA 668  
 DB 609 FEGTYEWEHMHMSDVAAAYFNLOIENSEDNKSTLSLQFVDSAADMPLAKHGAFTNWVA 668  
 QY 669 SKELQPGSARSTRHLEIPLKEASYQEGDHLGVIIPRYEGIVNRVTARFGLDASQIIRL 728  
 DB 669 SKELQPGSARSTRHLEIPLKEASYQEGDHLGVIIPRYEGIVNRVTARFGLDASQIIRL 728  
 QY 729 EABEEKLAHLPLAKTVSVEELLOYVELQDPVTRTQLRAMAATVCPHPKVELEALLEKQA 788  
 DB 729 EABEEKLAHLPLAKTVSVEELLOYVELQDPVTRTQLRAMAATVCPHPKVELEALLEKQA 788  
 QY 789 YKEQVLAKRLTLMLELEKYPACEMKFSFIALPSPRIRPRYSISSPRVDEKQASITVSV 848  
 DB 789 YKEQVLAKRLTLMLELEKYPACEMKFSFIALPSPRIRPRYSISSPRVDEKQASITVSV 848  
 QY 849 VSGEAWSGYGEYKGIASNYLAELQEGDITTCFISTPOSEFTLPKDPETPLIMVPGTGVA 908  
 DB 849 VSGEAWSGYGEYKGIASNYLAELQEGDITTCFISTPOSEFTLPKDPETPLIMVPGTGVA 908  
 QY 909 PFRGFGVQARKQLKEQSGSLGEAHLIFGCRSPHEDLYOELENAQSEGIITLHTAFSRMP 968  
 DB 909 PFRGFGVQARKQLKEQSGSLGEAHLIFGCRSPHEDLYOELENAQSEGIITLHTAFSRMP 968  
 QY 969 NQPKTYVQHVMEQDGKKLIELDDOGAHHFYICGDSQMAPAVEATLMKSYADHVQVSEADA 1028  
 DB 969 NQPKTYVQHVMEQDGKKLIELDDOGAHHFYICGDSQMAPAVEATLMKSYADHVQVSEADA 1028  
 QY 1029 RLWLOOLEEKGRYAKDVWAG 1048  
 DB 1029 RLWLOOLEEKGRYAKDVWAG 1048

309	QKUKYGVGVLINEALRWPAPAE	SLYAKEDTVLGGEYPLEKGBDELWVLLIQ	LDHDKTIMG	368
369	DDVEEERPERFENP	SAIQHAFKPFNGQGRACIGQOF	FALHEATLVLGMLMKHDFEDHTN	428
369	DDVEEERPERFENP	SAIQHAFKPFNGQGRACIGQOF	FALHEATLVLGMLMKHDFEDHTN	428
429	YELDIKETTLTKPEGFV	VVAKSKKIPLGIGTPSPSTEOSAKKVKRKAENAHNTPLLVLYGS	488	
429	YELDIKETTLTKPEGFV	VVAKSKKIPLGIGTPSPSTEOSAKKVKRKAENAHNTPLLVLYGS	488	
489	NMGTAEGTARDLADI	AMSKGFAQVATLDSHAGNLREGAVLIVTASYN	GHPDPNAKQFV	548
489	NMGTAEGTARDLADI	AMSKGFAQVATLDSHAGNLREGAVLIVTASYN	GHPDPNAKQFV	548
549	DWLDQASADBEVKG	VRYSVFCCGDKNATTVQKVPAFIDETLAAKGAENIADRGEADASDD	608	
549	DWLDQASADBEVKG	VRYSVFCCGDKNATTVQKVPAFIDETLAAKGAENIADRGEADASDD	608	
609	FECTYEERHMHMSD	VAAYFNLDIENSEDNKSTLSLQFVDSADMP	LAKMHGAFSTNVVA	668
609	FECTYEERHMHMSD	VAAYFNLDIENSEDNKSTLSLQFVDSADMP	LAKMHGAFSTNVVA	668
669	SKELQPGSARSTR	HLIEIELPKEAASYQEGDHLGVIPRNYEGIVNRVTARFGLDASQOIRL	728	
669	SKELQPGSARSTR	HLIEIELPKEAASYQEGDHLGVIPRNYEGIVNRVTARFGLDASQOIRL	728	
729	EAEFEELAHLP	LAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCP	PHKVELEALLKQA	788
729	EAEFEELAHLP	LAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCP	PHKVELEALLKQA	788
789	YKQSVLAKRLT	MLELLEKYPACEMKSEFTALLPSTRPRIYSISSSPRVDEKQASITVSV	848	
789	YKQSVLAKRLT	MLELLEKYPACEMKSEFTALLPSTRPRIYSISSSPRVDEKQASITVSV	848	
849	VSGEAMSGYGEYK	GIAISNYLAELOEGDTITCFISTPOSEFTLPKDPETPLIMVGPCTGVA	908	
849	VSGEAMSGYGEYK	GIAISNYLAELOEGDTITCFISTPOSEFTLPKDPETPLIMVGPCTGVA	908	
909	PFRGFVQARKLKEQ	QSGLGEAHLXFGCRSPHEDYLYQEBLENAQSEGITLHTAFSRMP	968	
909	PFRGFVQARKLKEQ	QSGLGEAHLXFGCRSPHEDYLYQEBLENAQSEGITLHTAFSRMP	968	
969	NQPKTVQHVMEQD	GKKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADHVQVSEADA	1028	
969	NQPKTVQHVMEQD	GKKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADHVQVSEADA	1028	
1029	RLWLOOLEEKGRY	AKDVWAG	1048	
1029	RLWLOOLEEKGRY	AKDVWAG	1048	
RESULT 9				
AA72208				
ID	AA772208 standard; Protein; 1049 AA.			
XX				
AC	AA772208;			
XX				
DT	24-APR-2001 (first entry)			

XX	Bacillus megaterium monooxygenase enzyme homologue, P450BM-3.
DE	
XX	
KW	Monooxygenase enzyme; P450BM-3 homologue; P450cam; oxidation;
KW	halogenated aromatic compound; electron transfer; putidaredoxin;
KW	putidaredoxin reductase; detoxification.
XX	
XX	Bacillus megaterium.
OS	
XX	
PN	WO200078973-A1.
XX	
PD	28-DEC-2000.
XX	
PF	19-JUN-2000; 2000WO-GB02379.

XX 18-JUN-1999; 99GB-0014373.  
 PR (ISIS-) ISIS INNOVATION LTD.  
 PA Wong LL, Jones JP;  
 PI WPI; 2001-071397/08.  
 XX N-PSDB; AAD02365.  
 XX  
 XX New process for detoxifying environments contaminated with halo  
 PT aromatic compounds comprises treating the affected area with a  
 PT monooxygenase enzyme -  
 PT  
 PS Disclosure; Page 32-39; 42pp; English.  
 XX  
 XX The present invention relates to a process for enzymatically oxidising  
 CC the halogenated aromatic compounds such as 1,2-dichlorobenzene,  
 CC 1,2,4-trichlorobenzene, 3,3'-dichlorobiphenyl or 2',4',5,  
 CC 5'-pentachlorobiphenyl. The process comprises treating the polluted  
 CC environment with a monooxygenase enzyme. A monooxygenase enzyme, p450cam,  
 CC and its physiological electron transfer partners, putidaredoxin and  
 CC putidaredoxin reductase, are used to oxidise the halogenated aromatic  
 CC compounds. Also mutants of the monooxygenase enzyme with substitutions in  
 CC the active site have enhanced oxidation activity. The process and the  
 CC transgenic plant or animal which expresses the monooxygenase enzyme are  
 CC used for detoxifying the environment polluted with the halo aromatic  
 CC compounds. The present sequence is a bacillus megaterium monooxygenase  
 CC enzyme, p450BM-3, which is homologous to the monooxygenase  
 CC enzyme, p450cam.  
 XX  
 SQ Sequence 1049 AA;  
 Query Match 80.7%; Score 846; DB 22; Length 1049;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TIKEMPQKTFGKLNPLINTDKPVQALMKIADLGEIFKFPAGRVTRYLSSQRLIKE 60  
 DB 2 TIKEMPQKTFGKLNPLINTDKPVQALMKIADLGEIFKFPAGRVTRYLSSQRLIKE 61  
 QY 61 ACDESFNLSQALQVRFDFAGDGLFTSWTHEKNKKAHNILLPFSQOAMGYHAMVY 120  
 DB 62 ACDESFNLSQALQVRFDFAGDGLFTSWTHEKNKKAHNILLPFSQOAMGYHAMVY 121  
 QY 121 DIAVLQVQWERLNADEHIEVPEDMTRLTDTGLCGFNFRNSFYRDQPHFITSMVRA 180  
 DB 122 DIAVLQVQWERLNADEHIEVPEDMTRLTDTGLCGFNFRNSFYRDQPHFITSMVRA 181  
 QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKITADRKASGEQSDLLTHMLNG 240  
 DB 182 LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKITADRKASGEQSDLLTHMLNG 241  
 QY 241 KDPETGEPLDENIRQITFTLAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLD 300  
 DB 242 KDPETGEPLDENIRQITFTLAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLD 301  
 QY 301 PVPYSYQVQKLVGVGNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPLQ 360  
 DB 302 PAFSYQVQKLVGVGNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPLQ 361  
 QY 361 HRDKTIWDDVEFRPERFENPSAIPQAFKPFNGQRCIGQOFALHEATLVLGMLKH 420  
 DB 362 HRDKTIWDDVEFRPERFENPSAIPQAFKPFNGQRCIGQOFALHEATLVLGMLKH 421  
 QY 421 FDEHDTNYELDKETITLTKPEGVVKAQSKKIPGLGIPSPSTEQSAKKVKKAEANAHT 480  
 DB 422 FDEHDTNYELDKETITLTKPEGVVKAQSKKIPGLGIPSPSTEQSAKKVKKAEANAHT 481  
 QY 481 PLLVLVCSNMGTAEGTARDLADIAMSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540  
 DB 482 PLLVLVCSNMGTAEGTARDLADIAMSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 541

QY 541 PDNAKOFVDWLQASADEVKGVRYSVFGCGDKNWTYQKVPFIDETLAAGAENIADR 600  
 DB 542 PDNAKOFVDWLQASADEVKGVRYSVFGCGDKNWTYQKVPFIDETLAAGAENIADR 601  
 QY 601 GEADASDDFEGTYEWEHREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 660  
 DB 602 GEADASDDFEGTYEWEHREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 661  
 QY 661 AFSTNVVASKELQPGSARSSTRHLELPELPEASVQEGDHLGVIPRNYEGVIVNRTARFGL 720  
 DB 662 AFSTNVVASKELQPGSARSSTRHLELPELPEASVQEGDHLGVIPRNYEGVIVNRTARFGL 721  
 QY 721 DASQQRLEAEAEKLAHLPLAKTVSVVEELQYVELQDPVTRTQLRAMAARTVCPPHKVEL 780  
 DB 722 DASQQRLEAEAEKLAHLPLAKTVSVVEELQYVELQDPVTRTQLRAMAARTVCPPHKVEL 781  
 QY 781 EALLEKQAYKEQVLAHRLMELLEKYPACEMKFSFIALLPISIRPRYYSISSPRVDEK 840  
 DB 782 EALLEKQAYKEQVLAHRLMELLEKYPACEMKFSFIALLPISIRPRYYSISSPRVDEK 841  
 QY 841 QASITVSVVSGEAWSGYGEYKGTASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900  
 DB 842 QASITVSVVSGEAWSGYGEYKGTASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 901  
 QY 901 VGPSTGVAPFRGFGVQARKQLKEQQLGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 960  
 DB 902 VGPSTGVAPFRGFGVQARKQLKEQQLGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 961  
 QY 961 HTAFSRMPNQPKTYVQHVMEQDKKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 DB 962 HTAFSRMPNQPKTYVQHVMEQDKKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021  
 QY 1021 HQVSEADARLWLOOLEKGRYAKDVWAG 1048  
 DB 1022 HQVSEADARLWLOOLEKGRYAKDVWAG 1049  
 RESULT 10  
 AAR11604  
 ID AAR11604 standard; Protein; 1085 AA.  
 XX AAR11604;  
 AC  
 XX  
 XX 20-JUN-1991 (first entry)  
 DT  
 XX  
 XX P450 17-alpha/p450 BM-3 fusion protein.  
 DE  
 XX bovine adrenal; cytochrome P450; oxidase; reductase; steroid;  
 KW plasmid p(alphaBm1).  
 XX JP03061490-A.  
 XX  
 XX 18-MAR-1991.  
 PD  
 XX  
 XX 28-JUL-1989; 89JP-0197296.  
 PF  
 XX  
 XX 28-JUL-1989; 89JP-0197296.  
 PR  
 XX  
 XX (SUMO ) SUMITOMO CHEM IND KK.  
 PA  
 XX  
 XX WPI; 1991-121848/17.  
 DR  
 XX  
 XX N-PSDB; AAQ11474.  
 DR  
 XX  
 XX P450 reductase fused oxidase coding gene - has both mono-atomic  
 PT oxygenation activity of bovine adrenal cytochrome p450 17-alpha  
 PT and reductivity supplying activity  
 XX  
 XX  
 PS Claim 1; Fig 2; 8pp; Japanese.  
 XX  
 CC The protein is a fusion of bovine adrenal cytochrome P450 17-alpha  
 CC and Bacillus megaterium-derived cytochrome P450 BM-3. The fusion  
 CC protein has the monoatomic oxygenation activity of the former and  
 CC the reductivity supplying activity of the latter. Plasmid p(alphaBm1),

CC containing the recombinant sequence encoding the fusion protein, is  
CC used to transform *Saccharomyces cerevisiae*. The transformant is  
CC designated AH22(p(alphaBM-1)) and can be used for the synthesis of  
CC steroids.

XX SQ Sequence 1085 AA;  
Query Match 25.4%; Score 266; DB 12; Length 1085;  
Best Local Similarity 100.0%; Pred. No. 5.9e-260;  
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 768 AAKTVCPPHKVEALELLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRP 827  
DB 806 AAKTVCPPHKVEALELLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRP 865  
QY 828 YSISSSPRVDEKQASITVSVSGEAWSGYGEVKGIAFNLAELQEGDTITCFISTPQSE 887  
DB 866 YSISSSPRVDEKQASITVSVSGEAWSGYGEVKGIAFNLAELQEGDTITCFISTPQSE 925  
QY 888 FTLPKDPETPLIMVPGTGVAPFRGFVQARKQKQGSGLGEAHLYFGCRSPHEDYLYQE 947  
DB 926 FTLPKDPETPLIMVPGTGVAPFRGFVQARKQKQGSGLGEAHLYFGCRSPHEDYLYQE 985  
QY 948 ELENAQSEGIITLHTAFSRMPNPKTYVOHVMEQDGKLIELLDQGAHYICGDSQMAP 1007  
DB 986 ELENAQSEGIITLHTAFSRMPNPKTYVOHVMEQDGKLIELLDQGAHYICGDSQMAP 1045  
QY 1008 AVEATLMKSYADVHVQVSEADARLWLQ 1033  
DB 1046 AVEATLMKSYADVHVQVSEADARLWLQ 1071

RESULT 11  
AA27545  
ID AA27545 standard; peptide; 17 AA.  
XX AC AA27545;  
DT 30-NOV-1999 (first entry)  
XX DE B. megaterium P-450BM-3 peptide fragment.  
XX KW Monoamine Oxidase; MAO; mutation; MAO B; cellular neurotransmitter;  
XX KW vasoamine; enzyme; human; P-450.  
XX OS Bacillus megaterium.  
XX PN WO9946297-A1.  
XX PD 16-SEP-1999.  
XX PF 10-MAR-1999; 99WO-US05173.  
XX PR 11-MAR-1998; 98US-0077482.  
XX PA (RERE-) RES DEV FOUND.  
XX PI Abell CW, Lewis DA;  
XX DR WPI; 1999-561665/47.  
XX PT New mutant enzyme useful for regulation of neurotransmitters -  
XX PS Example 1; Fig 1; 37pp; English.

CC The invention provides an isolated, mutated Monoamine Oxidase B (MAO B)  
CC enzyme having at least one amino acid substitution for wild-type amino  
CC acids in a MAO B active site, the wild-type amino acid residues selected  
CC from Phe423, Glu427 and Thr428. A plasmid containing the DNA encoding the  
CC mutated MAO B and regulatory elements can be used for the recombinant  
CC expression of the enzyme. The mutated MAO B enzyme is useful for indirect  
CC regulation of cellular neurotransmitters and vasoamines, as the  
CC substitutions reduce MAO B's activity and alters its pH profile. The

CC present sequence represents a B. megaterium P-450BM-3 peptide fragment.  
XX SQ Sequence 17 AA;  
Query Match 1.6%; Score 17; DB 20; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.6e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 ITFLIAGHETTSGLLSF 275  
DB 1 ITFLIAGHETTSGLLSF 17

RESULT 12  
AAR66738  
ID AAR66738 standard; Protein; 693 AA.  
XX AC AAR66738;  
DT 19-JUL-1995 (first entry)  
XX DE Cytochrome-P450-oxidoreductase.  
XX KW Cytochrome-P450-oxidoreductase; monooxygenase.  
XX OS Aspergillus niger ATCC 1015.  
XX PN WO9429453-A.  
XX PD 22-DEC-1994.  
XX PF 10-JUN-1994; 94WO-NL00135.  
XX PR 11-JUN-1993; 93NL-0001025.  
XX PA (NEDE) NEDERLANDSE ORG TOEGEPAST.  
XX PI Van DEN BRINK JM, Van GORCOM RF, Van GORCOM RFM;  
XX DR WPI; 1995-036481/05.  
XX DR N-PSDB; AAQ79914.  
XX PT Recombinant DNA mol. encoding cytochrome P450 oxidoreductase -  
XX PT esp. isolated from filamentous fungi, useful for increasing  
XX PT monooxygenase enzymatic conversion  
XX PS Disclosure; Fig. 2; 46pp; English.

CC The primers given in AAQ79915-19 were used for the PCR amplification  
CC of A. niger ATCC 1015 chromosomal DNA. These degenerate primers are  
CC based on conserved sequences in known cytochrome-P450-  
CC oxidoreductases. The DNA sequence of an isolated clone, given in  
CC AAQ79914, encodes a cytochrome-P450-oxidoreductase having the  
CC sequence given in AAR66738.

XX SQ Sequence 693 AA;

Query Match 1.4%; Score 15; DB 16; Length 693;  
Best Local Similarity 100.0%; Pred. No. 8.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVGGTGVAPFRGF 913  
DB 544 IMVGGTGVAPFRGF 558

RESULT 13  
AAB49682  
ID AAB49682 standard; Protein; 597 AA.  
XX AC AAB49682;  
DT 03-APR-2001 (first entry)



XX DE Human reductase amino acid sequence.  
 XX KW Human; reductase; flavoprotein; cytochrome p450 reductase; chromosome 9;  
 KW KW nitric oxide synthase; cancer; drug bioactivation.  
 XX OS Homo sapiens.  
 XX PN WO200077180-A1.  
 XX PD 21-DEC-2000.  
 XX PF 13-JUN-2000; 2000WO-US16245.  
 XX PR 16-JUN-1999; 99US-0334490.  
 XX PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX PI Powell DJ, Tew DG;  
 XX DR WPI: 2001-112221/12.  
 XX DR N-PSDB; AAF29129.  
 XX PT New isolated reductase polypeptides and polynucleotides, useful in  
 PT screening assays, particularly for diagnosing a disease associated with  
 PT altered levels of reductase and as vaccines to protect an individual  
 PT against these diseases -  
 XX PS Claim 1; Page 25-26; 27pp; English.  
 XX CC The present invention relates to DNA sequence AAF29129 which encodes a  
 CC human reductase represented in AAB49682. The DNA sequence shows homology  
 CC with nucleotide sequences of cytochrome p450 reductases and nitric oxide  
 CC synthases. The protein is related to members of the FNR family of  
 CC flavoproteins. This reductase gene maps to human chromosome 9. The  
 CC reductase polypeptide and polynucleotide are useful in screening assays,  
 CC particularly as diagnostic reagents for detecting abnormally decreased or  
 CC increased levels of the reductase polypeptide or mRNA expression. In  
 CC particular, these are useful for diagnosing or determining susceptibility  
 CC of a subject to a disease associated with altered levels of reductase  
 CC polypeptide. Diseases which may be treated by methods using the reductase  
 CC include cancer, and the sequences may be used in methods for drug  
 CC bioactivation. The polypeptides and polynucleotides may also be used as  
 CC vaccines to protect an individual against these diseases. The polypeptide  
 CC or its fragments are also useful as immunogens to produce antibodies that  
 CC are immunospecific for the reductase polypeptides. The polynucleotide  
 CC sequences may also be used in chromosome localization studies and tissue  
 CC expression studies.  
 XX SQ Sequence 597 AA;  
 Query Match 1.28; Score 13; DB 22; Length 597;  
 Best Local Similarity 100.0%; Pred. No. 0.00081;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 899 IMVGPGRGVAPFR 911  
 Db 454 IMVGPGRGVAPFR 466  
 RESULT 14  
 AAY33673  
 ID AAY33673 standard; Protein; 700 AA.  
 XX AC AAY33673;  
 XX DT 07-JAN-2000 (first entry)  
 XX DE B. bassiana POPS reductase protein.  
 XX KW POPS; 2-phenoxypropionic acid; 2-(4-hydroxyphenoxy) propionic acid;  
 KW herbicide intermediate; hydroxylation rate; reductase.  
 XX PI Gillam EJ, Notley LM, Devoss J, Guengerich FP, Volkov A;  
 XX

OS Beauveria bassiana.  
 XX DE19814528-A1.  
 XX PD 07-OCT-1999.  
 XX PF 01-APR-1998; 98DE-1014528.  
 XX PR 01-APR-1998; 98DE-1014528.  
 XX PA (BADI ) BASF AG.  
 XX PI Hauer B, Dingler C, Van Gorcom R, Van Zeijl C;  
 XX DR WPI: 1999-552253/47.  
 XX DR N-PSDB; AAZ23663.  
 XX PT Production of 2-(4-hydroxyphenoxy) propionic acid from  
 PT 2-phenoxypropionic acid using microorganism having increased  
 PT hydroxylation rate -  
 XX PS Example 5; Page 28-31; 36pp; German.  
 XX CC This invention describes a novel method for the production of  
 CC 2-(4-hydroxyphenoxy) propionic acid (I) from 2-phenoxypropionic acid  
 CC (POPS) or its salts. The method comprises a microorganism containing at  
 CC least one of the genes contained within a Beauveria bassiana genomic  
 CC sequence of 11292 bp (I), with two open reading frames. (I) is useful  
 CC as a herbicide intermediate. Microorganisms containing multiple copies of  
 CC (I) have significantly increased hydroxylation rates. This sequence  
 CC represents the Beauveria bassiana POPS reductase described in the method  
 CC of the invention.  
 XX SQ Sequence 700 AA;  
 Query Match 1.28; Score 13; DB 20; Length 700;  
 Best Local Similarity 100.0%; Pred. No. 0.00093;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 899 IMVGPGRGVAPFR 911  
 Db 541 IMVGPGRGVAPFR 553  
 RESULT 15  
 AAB73901  
 ID AAB73901 standard; Protein; 677 AA.  
 XX AC AAB73901;  
 XX DT 22-MAY-2001 (first entry)  
 XX DE Human derived cytochrome P450 reductase.  
 XX KW Human; cytochrome P450 monooxygenase; cytochrome P450 reductase; NPR;  
 KW pigment production; indole; dye; cosmetic industry; marker.  
 XX OS Homo sapiens.  
 XX PN WO200114565-A1.  
 XX PD 01-MAR-2001.  
 XX PF 11-AUG-2000; 2000WO-AU00966.  
 XX PR 11-AUG-1999; 99AU-0002156.  
 XX PA (UYOU ) UNIV QUEENSLAND.  
 XX PA (UYVA-) UNIV VANDERBILT.  
 XX PA (CALI ) CALIFORNIA INST OF TECHNOLOGY.  
 XX PI Gillam EJ, Notley LM, Devoss J, Guengerich FP, Volkov A;  
 XX

DR WPI; 2001-257635/26.  
DR N-PSDB; AAF76960.  
XX Generation of genetically modified cell to produce pigment -  
PT  
XX  
PS Claim 39; Page 145-148; 178pp; English.  
XX  
XX The present sequence is cytochrome P450 reductase. The invention  
CC relates to a method for producing pigment using cells containing  
CC cytochrome P450 sequences. It involves the use of genetic material  
CC encoding a cytochrome P450 protein or a functional derivative or  
CC homologue of it in the generation of a genetically modified cell. The  
CC cell has the capacity to produce a pigment in the presence of indole,  
CC or a precursor, analogue or derivative of indole, upon expression of  
CC the genetic material. Pigment from plant or plant material is useful  
CC in the dye or cosmetic industry or as commercial tags or as markers for  
CC transformation of microbial, plant or animal cells.  
XX  
SQ Sequence 677 AA;  
Query Match 1.1%; Score 12; DB 22; Length 677;  
Best Local Similarity 100.0%; Pred. No. 0.0093;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 899 IMVPGGTGVAPF 910  
| | | | | | | | | |  
Db 529 IMVPGGTGVAPF 540

Search completed: May 29, 2003, 08:41:38  
Job time : 78 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 29, 2003, 08:27:11 ; Search time 29 Seconds  
(without alignments)  
1063.284 Million cell updates/sec

Title: US-10-031-146-2  
Perfect score: 1048  
Sequence: 1 TIKEMPQKTFGLKNLPL.....RLWLQLEKGRYKDVWAG 1048

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	1.9	20	4	US-09-057-897-30
2	17	1.6	17	4	US-09-265-653-20
3	15	1.4	693	1	US-08-553-279-2
4	10	1.0	588	4	US-09-627-216A-14
5	10	1.0	629	4	US-09-134-001C-4394
6	10	1.0	1429	1	US-07-642-002-2
7	10	1.0	1429	2	US-08-365-486A-13
8	10	1.0	1429	2	US-08-319-866-11
9	10	1.0	1429	4	US-08-880-342-13
10	10	1.0	1430	2	US-08-705-625-4
11	10	1.0	1430	3	US-09-010-998-5
12	10	1.0	1430	4	US-09-220-574-4
13	10	1.0	1433	2	US-08-365-486A-21
14	10	1.0	1433	4	US-09-123-708-4
15	10	1.0	1433	4	US-09-123-624-4
16	10	1.0	1433	4	US-08-880-342-21
17	10	1.0	1434	2	US-08-365-486A-19
18	10	1.0	1434	4	US-08-880-342-19
19	10	1.0	1554	2	US-08-705-625-3
20	10	1.0	1554	3	US-09-010-998-6
21	10	1.0	1554	4	US-09-220-574-3
22	9	0.9	679	4	US-09-302-620B-83
23	9	0.9	679	4	US-09-302-620B-84
24	9	0.9	1144	1	US-08-147-812-5
25	9	0.9	1144	2	US-08-319-866-12
26	9	0.9	1144	4	US-09-123-708-2
27	9	0.9	1144	4	US-09-123-624-2

28 8 0.8 406 6 5212296-6 Patent No. 5212296  
29 8 0.8 412 1 US-08-102-863-11 Sequence 11, Appl  
30 8 0.8 412 5 PCT-US92-10885-11 Sequence 11, Appl  
31 8 0.8 504 1 US-08-457-274A-25 Sequence 25, Appl  
32 8 0.8 504 5 PCT-US95-05758-25 Sequence 25, Appl  
33 8 0.8 505 4 US-09-627-216A-12 Sequence 12, Appl  
34 8 0.8 505 4 US-09-126-420A-22 Sequence 22, Appl  
35 8 0.8 513 4 US-09-351-229-4 Sequence 4, Appl  
36 8 0.8 576 3 US-08-948-564-16 Sequence 16, Appl  
37 8 0.8 1350 2 US-08-319-866-9 Sequence 9, Appl  
38 7 0.7 29 4 US-09-082-358B-34 Sequence 34, Appl  
39 7 0.7 33 2 US-08-511-872-4 Sequence 4, Appl  
40 7 0.7 33 2 US-08-511-872-6 Sequence 6, Appl  
41 7 0.7 33 2 US-08-511-872-9 Sequence 9, Appl  
42 7 0.7 33 2 US-08-511-872-10 Sequence 10, Appl  
43 7 0.7 33 2 US-08-511-872-11 Sequence 11, Appl  
44 7 0.7 103 3 US-08-894-173-77 Sequence 77, Appl  
45 7 0.7 103 4 US-09-398-193-77 Sequence 77, Appl

## ALIGNMENTS

RESULT 1  
US-09-057-897-30  
; Sequence 30, Application US/09057897  
; Patent No. 6300476  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Anthony Y.H.  
; TITLE OF INVENTION: Anti-Peptide Antibody Against Human  
; TITLE OF INVENTION: Cytochrome P450 3A4  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: US  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,897  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hand, J. Mark  
; REGISTRATION NUMBER: 36,545  
; REFERENCE/DOCKET NUMBER: 19902  
; TELEPHONE: (732)594-3905  
; TELEFAX: (732)594-4720  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-057-897-30

Query Match 1.9%; Score 20; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 VDKIIADRKASGQSDLLT 235  
Db 1 VDKIIADRKASGQSDLLT 20

## RESULT 2

US-09-265-653-20  
; Sequence 20, Application US/09265653  
; Patent No. 6451570  
; GENERAL INFORMATION:  
; APPLICANT: Abeil, Creed W.  
; APPLICANT: Lewis, Duane A.  
; TITLE OF INVENTION: Mutants of Monoamine Oxidase B  
; FILE REFERENCE: D6048  
; CURRENT APPLICATION NUMBER: US/09/265,653  
; CURRENT FILING DATE: 1999-03-10  
; EARLIER APPLICATION NUMBER: US 60/077,482  
; EARLIER FILING DATE: 1998-03-11  
; NUMBER OF SEQ ID NOS: 27  
; SEQ ID NO 20  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Bacillus megaterium  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence containing conserved site of  
; OTHER INFORMATION: Bacillus megaterium P-450BM3  
US-09-265-653-20

Query Match 1.6%; Score 17; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 ITFLIAGHETTSGLLSF 275  
Db 1 ITFLIAGHETTSGLLSF 17  
|||||

## RESULT 3

US-08-553-279-2  
; Sequence 2, Application US/08553279  
; Patent No. 5801024  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: No. 5801024el oxidoreductase from filamentous funghi,  
; TITLE OF INVENTION: DNA coding therefore and cells transformed with said DNA.  
; NUMBER OF SEQUENCES: 9  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/553,279  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP PCT/NL94/00135  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 693 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
US-08-553-279-2

Query Match 1.4%; Score 15; DB 1; Length 693;  
Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVGPCTGVAPPRGF 913  
Db 544 INVGPCTGVAPPRGF 558  
|||||

## RESULT 4

US-09-627-216A-14  
; Sequence 14, Application US/09627216A  
; Patent No. 6368837  
; GENERAL INFORMATION:  
; APPLICANT: Sariaslani, Sima F  
; APPLICANT: Tang, Xiao-Song  
; APPLICANT: Qi, Wei Wei  
; APPLICANT: Vannelli, Todd  
; APPLICANT: Gatenby, Anthony  
; TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid  
; FILE REFERENCE: BC1009 US NA  
; CURRENT APPLICATION NUMBER: US/09/627,216A  
; CURRENT FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 60/147,719  
; PRIOR FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 14  
; LENGTH: 588  
; TYPE: PRT  
; ORGANISM: Helianthus tuberosus  
US-09-627-216A-14

Query Match 1.0%; Score 10; DB 4; Length 588;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSISSSP 835  
Db 365 PRYSISSSP 374  
|||||

## RESULT 5

US-09-134-001C-4394  
; Sequence 4394, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4394  
; LENGTH: 629  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4394

Query Match 1.0%; Score 10; DB 4; Length 629;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 902 GPGTGVAFFR 911  
Db 489 GPGTGVAFFR 498  
|||||

## RESULT 6

US-07-642-002-2  
; Sequence 2, Application US/07642002  
; Patent No. 5268465  
; GENERAL INFORMATION:  
; APPLICANT: Bredt, David S.  
; APPLICANT: Hwang, Paul M.  
; APPLICANT: Reed, Randall  
; APPLICANT: Snyder, Solomon H.

;; TITLE OF INVENTION: Purification and Molecular Cloning of Nitric  
;; TITLE OF INVENTION: Oxide Synthase  
;; NUMBER OF SEQUENCES: 2  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Banner, Birch, McKie & Beckett  
;; STREET: One Thomas Circle, NW  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.24  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/642,002  
;; FILING DATE: 19910118  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Kagan, Sarah A.  
;; REGISTRATION NUMBER: 32,141  
;; REFERENCE/DOCKET NUMBER: 1107.033576  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 296-3500  
;; TELEFAX: (202) 296-7830  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1429 amino acids  
;; TYPE: AMINO ACID  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-07-642-002-2

Query Match 1.0%; Score 10; DB 1; Length 1429;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYISISSP 835  
Db 1172 PRYISISSP 1181

RESULT 7  
US-08-365-486A-13  
;; Sequence 13, Application US/08365486A  
;; Patent No. 5834306  
;; GENERAL INFORMATION:  
;; APPLICANT: Webster, Keith A.  
;; APPLICANT: Bishopric, Nanette H.  
;; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
;; TITLE OF INVENTION: Therapeutic Constructs  
;; NUMBER OF SEQUENCES: 31  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Dehlinger & Associates  
;; STREET: 350 Cambridge Avenue, Suite 250  
;; CITY: Palo Alto  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 94306  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/365,486A  
;; FILING DATE: 23-DEC-1994  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sholtz, Charles K.  
;; REGISTRATION NUMBER: 38,615  
;; REFERENCE/DOCKET NUMBER: 8255-0018

;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 324-0880  
;; TELEFAX: (415) 324-0960  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1429 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-365-486A-13

Query Match 1.0%; Score 10; DB 2; Length 1429;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYISISSP 835  
Db 1172 PRYISISSP 1181

RESULT 8  
US-08-319-866-11  
;; Sequence 11, Application US/08319866  
;; Patent No. 5929223  
;; GENERAL INFORMATION:  
;; APPLICANT: Tully, Timothy P.  
;; APPLICANT: Yin, Jerry C.  
;; APPLICANT: Regulski, Michael  
;; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES  
;; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY  
;; NUMBER OF SEQUENCES: 24  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
;; STREET: Two Militia Drive  
;; CITY: Lexington  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02173  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/319,866  
;; FILING DATE: 7-OCT-1994  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Granahan, Patricia  
;; REGISTRATION NUMBER: 32,227  
;; REFERENCE/DOCKET NUMBER: CSHL94-03  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 861-6240  
;; TELEFAX: (617) 861-9540  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1429 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-319-866-11

Query Match 1.0%; Score 10; DB 2; Length 1429;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYISISSP 835  
Db 1172 PRYISISSP 1181

## RESULT 9

US-08-880-342-13  
; Sequence 13, Application US/08880342  
; Patent No. 6218179  
; GENERAL INFORMATION:  
; APPLICANT: Webster, Keith A.  
; APPLICANT: Bishopric, Nanette H.  
; APPLICANT: Murphy, Brian  
; APPLICANT: Laderoute, Keith R.  
; APPLICANT: Green, Christopher J.  
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
; TITLE OF INVENTION: Therapeutic Constructs  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/880,342  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/IB95/00996  
; FILING DATE: 13-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/365,486  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 8255-0018.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1429 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-880-342-13

Query Match 1.0%; Score 10; DB 4; Length 1429;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSISSP 835  
Db 1172 PRYSSISSP 1181

## RESULT 10

US-08-705-625-4  
; Sequence 4, Application US/08705625  
; Patent No. 5908756  
; GENERAL INFORMATION:  
; APPLICANT: Snyder, Solomon H.  
; APPLICANT: Jaffrey, Samie R.  
; TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric  
; TITLE OF INVENTION: Oxide Synthase  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Banner & Witcoff

STREET: 1001 G Street, N.W.  
CITY: Washington, D.C.  
COUNTRY: U.S.A.  
ZIP: 20001-4597  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/705,625  
; FILING DATE: 30-AUG-1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.57071  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1430 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-705-625-4

Query Match 1.0%; Score 10; DB 2; Length 1430;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSISSP 835  
Db 1172 PRYSSISSP 1181

## RESULT 11

US-09-010-998-5  
; Sequence 5, Application US/09010998  
; Patent No. 6103872  
; GENERAL INFORMATION:  
; APPLICANT: Snyder, Solomon  
; APPLICANT: Jaffrey, Samie  
; APPLICANT: Snowman, Adele  
; APPLICANT: Eliasson, Mikael  
; APPLICANT: Cohen, No. 6103872m  
; TITLE OF INVENTION: CAPON, a protein that binds  
; TITLE OF INVENTION: neuronal nitric oxide synthase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Banner & Witcoff  
; STREET: 1001 G Street, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/010,998  
; FILING DATE: 22-JAN-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A  
REGISTRATION NUMBER: 32141  
REFERENCE/DOCKET NUMBER: 01107.73424  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX:

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1430 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6103872e  
US-09-010-998-5

Query Match 1.0%; Score 10; DB 3; Length 1430;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSSP 835  
| | | | | | | | | |  
Db 1172 PRYSSSSP 1181

## RESULT 12

US-09-220-574-4

Sequence 4, Application US/09220574  
Patent No. 6168926

## GENERAL INFORMATION:

APPLICANT: Snyder, Solomon H.

APPLICANT: Jaffrey, Samie R.

TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric

TITLE OF INVENTION: Oxide Synthase

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner &amp; Witcoff

STREET: 1001 G Street, N.W.

CITY: Washington, D.C.

COUNTRY: U.S.A.

ZIP: 20001-4597

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/220,574

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,625

FILING DATE: 30-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.57071

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1430 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-09-220-574-4  
Query Match 1.0%; Score 10; DB 4; Length 1430;  
Best Local Similarity 100.0%; Pred. No. 0.79;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 826 PRYSSSSP 835  
| | | | | | | | | |  
Db 1172 PRYSSSSP 1181

## RESULT 13

US-08-365-486A-21

Sequence 21, Application US/08365486A

Patent No. 5834306

## GENERAL INFORMATION:

APPLICANT: Webster, Keith A.

APPLICANT: Bishopric, Nanette H.

TITLE OF INVENTION: Tissue Specific Hypoxia Regulated

TITLE OF INVENTION: Therapeutic Constructs

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger &amp; Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/365,486A

FILING DATE: 23-DEC-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 8255-0018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 1433 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-365-486A-21

Query Match 1.0%; Score 10; DB 2; Length 1433;

Best Local Similarity 100.0%; Pred. No. 0.79;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 826 PRYSSSSP 835  
| | | | | | | | | |  
Db 1176 PRYSSSSP 1185

## RESULT 14

US-09-123-708-4

Sequence 4, Application US/09123708

Patent No. 6146887

## GENERAL INFORMATION:

APPLICANT: Schrader, Juergen

APPLICANT: GODECKE, Axel

TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC

TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS

FILE REFERENCE: 511169-2003

CURRENT APPLICATION NUMBER: US/09/123,708

CURRENT FILING DATE: 1998-07-28

EARLIER APPLICATION NUMBER: 08/553,503

EARLIER FILING DATE: 1996-03-01

EARLIER APPLICATION NUMBER: P4411402.8

EARLIER FILING DATE: 1994-03-31

; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1433  
; TYPE: PRT  
; ORGANISM: Cytomegalovirus  
US-09-123-708-4

Query Match 1.0%; Score 10; DB 4; Length 1433;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYISISSP 835  
| | | | | | | | | |  
Db 1176 PRYISISSP 1185

RESULT 15  
US-09-123-624-4  
; Sequence 4, Application US/09123624  
; Patent No. 6149936  
; GENERAL INFORMATION:  
; APPLICANT: SCHRADER, Jurgen  
; APPLICANT: GODECKE, Axel  
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC  
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
; FILE REFERENCE: 511169-2004  
; CURRENT APPLICATION NUMBER: US/09/123,624  
; CURRENT FILING DATE: 1998-07-28  
; PRIOR APPLICATION NUMBER: 08/553,503  
; PRIOR FILING DATE: 1996-03-01  
; PRIOR APPLICATION NUMBER: 4411402.8  
; PRIOR FILING DATE: 1994-03-31  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1433  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-123-624-4

Query Match 1.0%; Score 10; DB 4; Length 1433;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYISISSP 835  
| | | | | | | | | |  
Db 1176 PRYISISSP 1185

Search completed: May 29, 2003, 08:32:17  
Job time : 30 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:30:56 ; Search time 54 Seconds  
(without alignments)  
1964.489 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 1048

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Scoring table: OLIGO

Gapop 60.0 , Capext 60.0

Searched: 383519 seqs, 101223694 residues

Word size : 0

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published\_Applications\_AA:

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*
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- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB pep.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	1.6	17	9	US-10-119-604C-20
2	13	1.2	597	9	US-09-778-319-2
3	12	1.1	677	9	US-09-371-347-23
4	10	1.0	588	10	US-09-765-873A-14
5	10	1.0	1433	9	US-10-224-249-14
6	9	0.9	516	10	US-09-740-046-4
7	9	0.9	679	9	US-10-138-838-83
8	9	0.9	679	9	US-10-138-838-84
9	9	0.9	679	9	US-10-138-838-117
10	9	0.9	679	9	US-10-138-838-118
11	9	0.9	679	9	US-10-139-031-83
12	9	0.9	679	9	US-10-139-031-84
13	9	0.9	679	9	US-10-139-031-117
14	9	0.9	679	9	US-10-139-031-118
15	9	0.9	679	9	US-10-138-905-83
16	9	0.9	679	9	US-10-138-905-84
17	9	0.9	679	9	US-10-138-905-117
18	9	0.9	679	9	US-10-138-905-118
19	9	0.9	679	9	US-10-138-916-83

20 9 0.9 679 9 US-10-138-916-84 Sequence 84, Appl  
21 9 0.9 679 9 US-10-138-916-117 Sequence 117, App  
22 9 0.9 679 9 US-10-138-916-118 Sequence 118, App  
23 9 0.9 679 9 US-09-976-800-83 Sequence 83, Appl  
24 9 0.9 679 9 US-09-976-800-84 Sequence 84, Appl  
25 9 0.9 679 9 US-09-976-800-117 Sequence 117, App  
26 9 0.9 679 9 US-09-976-800-118 Sequence 118, App  
27 9 0.9 679 10 US-09-911-781-11 Sequence 11, Appl  
28 9 0.9 1144 9 US-09-870-759-124 Sequence 124, App  
29 8 0.8 361 10 US-09-854-122-43 Sequence 43, Appl  
30 8 0.8 362 10 US-09-854-122-42 Sequence 42, Appl  
31 8 0.8 505 10 US-09-765-873A-12 Sequence 12, Appl  
32 8 0.8 517 10 US-09-854-122-45 Sequence 45, Appl  
33 8 0.8 519 10 US-09-854-122-44 Sequence 44, Appl  
34 8 0.8 682 9 US-09-371-347-22 Sequence 22, Appl  
35 8 0.8 689 9 US-09-371-347-48 Sequence 48, Appl  
36 8 0.8 697 9 US-09-371-347-46 Sequence 46, Appl  
37 8 0.8 698 9 US-09-371-347-2 Sequence 2, Appl  
38 8 0.8 698 9 US-09-371-347-21 Sequence 21, Appl  
39 8 0.8 698 9 US-09-371-347-42 Sequence 42, Appl  
40 8 0.8 698 9 US-09-371-347-44 Sequence 44, Appl  
41 7 0.7 7 9 US-10-145-415-43 Sequence 43, Appl  
42 7 0.7 9 9 US-10-145-415-49 Sequence 49, Appl  
43 7 0.7 23 10 US-09-864-761-47602 Sequence 47602, A  
44 7 0.7 48 9 US-09-984-245-214 Sequence 214, App  
45 7 0.7 48 9 US-09-966-262-214 Sequence 214, App

#### ALIGNMENTS

##### RESULT 1

US-10-119-604C-20  
; Sequence 20, Application US/10119604C  
; Publication No. US20030082772A1  
; GENERAL INFORMATION:  
; APPLICANT: Abell, Creed W.  
; APPLICANT: Lewis, Duane A.  
; TITLE OF INVENTION: Mutants of Monoamine Oxidase B  
; FILE REFERENCE: D6048/D  
; CURRENT APPLICATION NUMBER: US/10119,604C  
; CURRENT FILING DATE: 2002-04-10  
; PRIOR APPLICATION NUMBER: US 09/265,653  
; PRIOR FILING DATE: 1998-03-10  
; NUMBER OF SEQ ID NOS: 27  
; SEQ ID NO 20  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Bacillus megaterium  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of active site of wild type  
; OTHER INFORMATION: P-450BM-3 enzyme  
US-10-119-604C-20

Query Match 1.6%; Score 17; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.8e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 ITFLIAGHETTSGLLSF 275

Db 1 ITFLIAGHETTSGLLSF 17

##### RESULT 2

US-09-778-319-2  
; Sequence 2, Application US/09778319  
; Patent No. US20020155560A1  
; GENERAL INFORMATION:  
; APPLICANT: POWELL, DAVID J.  
; APPLICANT: TEW, DAVID G.  
; TITLE OF INVENTION: A REDUCTASE  
; FILE REFERENCE: GH-70627-C1  
; CURRENT APPLICATION NUMBER: US/09/778,319

; CURRENT FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 09/334,490  
; PRIOR FILING DATE: 1999-06-16  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 597  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-778-319-2

Query Match 1.2%; Score 13; DB 9; Length 597;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPR 911  
Db 454 IMVPGTGVAPR 466

RESULT 3  
US-09-371-347-23  
; Sequence 23, Application US/09371347  
; Publication No. US20030082676A1  
; GENERAL INFORMATION:  
; APPLICANT: Roy A. Gravel et al.  
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;  
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE  
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER  
; FILE REFERENCE: 50004/003003  
; CURRENT APPLICATION NUMBER: US/09/371,347  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 60/071,622  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: 09/232,028  
; PRIOR FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 677  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-371-347-23

Query Match 1.1%; Score 12; DB 9; Length 677;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPR 910  
Db 529 IMVPGTGVAPR 540

RESULT 4  
US-09-765-873A-14  
; Sequence 14, Application US/09765873A  
; Patent No. US20010053847A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Xiao-Song  
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID  
; FILE REFERENCE: BC1009 US CIP  
; CURRENT APPLICATION NUMBER: US/09/765,873A  
; CURRENT FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: US/09/627,216  
; PRIOR FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: US 60/147,719  
; PRIOR FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 14  
; LENGTH: 588  
; TYPE: PRT  
; ORGANISM: Helianthus tuberosus

US-09-765-873A-14

Query Match 1.0%; Score 10; DB 10; Length 588;  
Best Local Similarity 100.0%; Pred. No. 0.77; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSSP 835  
Db 365 PRYSSSSP 374

RESULT 5  
US-10-224-249-14  
; Sequence 14, Application US/10224249  
; Publication No. US20030087867A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogels, Ronald V.  
; APPLICANT: Verlinden, Stefan F.F.  
; TITLE OF INVENTION: Gene therapy for enhancing and/or inducing angiogenesis  
; FILE REFERENCE: 2183-5233US  
; CURRENT APPLICATION NUMBER: US/10/224,249  
; CURRENT FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: PCT/NL00/00482  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: EP 9920263.2  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/143,101  
; PRIOR FILING DATE: 1999-07-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 1433  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CHAIN  
; LOCATION: (1)..(1433)  
; OTHER INFORMATION: Human nitric oxide synthase  
US-10-224-249-14

Query Match 1.0%; Score 10; DB 9; Length 1433;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSSP 835  
Db 1176 PRYSSSSP 1185

RESULT 6  
US-09-740-046-4  
; Sequence 4, Application US/09740046  
; Patent No. US20020009751A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN MET  
; FILE REFERENCE: METHODS OF USE  
; FILE REFERENCE: EX00-044C  
; CURRENT APPLICATION NUMBER: US/09/740,046  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/172,484  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: 60/172,482  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: 60/178,411  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: 60/191,881  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: 60/192,142  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4

LENGTH: 516  
TYPE: PRP  
ORGANISM: Drosophila melanogaster  
US-09-740-046-4

Query Match 0.9%; Score 9; DB 10; Length 516;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 374 FRPERFNP 382  
Db 416 FRPERFNP 424

RESULT 7  
US-10-138-838-83  
Sequence 83, Application US/10138838  
Publication No. US20030049821A1

GENERAL INFORMATION:  
APPLICANT: Wilson, Ron C.  
APPLICANT: Craft, David L.  
APPLICANT: Eirich, Dudley  
APPLICANT: Eshoo, Mark  
APPLICANT: Madduri, Krishna M.  
APPLICANT: Cornett, Cathy A.  
APPLICANT: Brenner, Alfred A.  
APPLICANT: Tang, Maria  
APPLICANT: Loper, John C.  
APPLICANT: Gleeson, Martin

TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
TITLE OF INVENTION: P450 OXIDOREDUCTASE

TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF  
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO

FILE REFERENCE: 1010-16  
CURRENT APPLICATION NUMBER: US/10/138,838

CURRENT FILING DATE: 2002-05-03  
PRIOR FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 83  
LENGTH: 679  
TYPE: PRP

ORGANISM: CANDIDATROPICALIS  
US-10-138-838-83

Query Match 0.9%; Score 9; DB 9; Length 679;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 PRYSSISS 834  
Db 437 PRYSSISS 445

RESULT 8  
US-10-138-838-84  
Sequence 84, Application US/10138838  
Publication No. US20030049821A1

GENERAL INFORMATION:  
APPLICANT: Wilson, Ron C.  
APPLICANT: Craft, David L.  
APPLICANT: Eirich, Dudley  
APPLICANT: Eshoo, Mark  
APPLICANT: Madduri, Krishna M.  
APPLICANT: Cornett, Cathy A.  
APPLICANT: Brenner, Alfred A.  
APPLICANT: Tang, Maria  
APPLICANT: Loper, John C.  
APPLICANT: Gleeson, Martin

TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
TITLE OF INVENTION: P450 OXIDOREDUCTASE

TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF

TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO  
FILE REFERENCE: 1010-16  
CURRENT APPLICATION NUMBER: US/10/138,838  
CURRENT FILING DATE: 2002-05-03

PRIOR FILING DATE: 2001-10-12  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 84  
LENGTH: 679  
TYPE: PRP

ORGANISM: CANDIDATROPICALIS  
US-10-138-838-84

Query Match 0.9%; Score 9; DB 9; Length 679;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 PRYSSISS 834  
Db 437 PRYSSISS 445

RESULT 9  
US-10-138-838-117  
Sequence 117, Application US/10138838  
Publication No. US20030049821A1

GENERAL INFORMATION:  
APPLICANT: Wilson, Ron C.  
APPLICANT: Craft, David L.  
APPLICANT: Eirich, Dudley  
APPLICANT: Eshoo, Mark  
APPLICANT: Madduri, Krishna M.  
APPLICANT: Cornett, Cathy A.  
APPLICANT: Brenner, Alfred A.  
APPLICANT: Tang, Maria  
APPLICANT: Loper, John C.  
APPLICANT: Gleeson, Martin

TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
TITLE OF INVENTION: P450 OXIDOREDUCTASE

TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX O  
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO

FILE REFERENCE: 1010-16  
CURRENT APPLICATION NUMBER: US/10/138,838

CURRENT FILING DATE: 2002-05-03  
PRIOR FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 117  
LENGTH: 679  
TYPE: PRP

ORGANISM: CANDIDATROPICALIS  
US-10-138-838-117

Query Match 0.9%; Score 9; DB 9; Length 679;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 PRYSSISS 834  
Db 437 PRYSSISS 445

RESULT 10  
US-10-138-838-118  
Sequence 118, Application US/10138838  
Publication No. US20030049821A1

GENERAL INFORMATION:  
APPLICANT: Wilson, Ron C.  
APPLICANT: Craft, David L.  
APPLICANT: Eirich, Dudley  
APPLICANT: Eshoo, Mark

```

; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,838
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-10-138-838-118

Query Match          0.9%; Score 9; DB 9; Length 679;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      826 PRYSSSS 834
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Db      437 PRYSSSS 445

RESULT 11
US-10-139-031-83
; Sequence 83, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Erich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,031
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-10-139-031-83

Query Match          0.9%; Score 9; DB 9; Length 679;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      826 PRYSSSS 834
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Db      437 PRYSSSS 445

RESULT 12
US-10-139-031-84
; Sequence 84, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Erich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,031
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-10-139-031-84

Query Match          0.9%; Score 9; DB 9; Length 679;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      826 PRYSSSS 834
      |||||
Db      437 PRYSSSS 445

RESULT 13
US-10-139-031-117
; Sequence 117, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Erich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,031
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-10-139-031-117
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Query Match 0.9%; Score 9; DB 9; Length 679;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSISS 834  
 Db 437 PRYSSISS 445

RESULT 14

US-10-139-031-118  
 ; Sequence 118, Application US/10139031  
 ; Publication No. US20030049822A1

; GENERAL INFORMATION:  
 ; APPLICANT: Wilson, Ron C.  
 ; APPLICANT: Craft, David L.  
 ; APPLICANT: Eirich, Dudley  
 ; APPLICANT: Eshoo, Mark  
 ; APPLICANT: Madduri, Krishna M.  
 ; APPLICANT: Cornett, Cathy A.  
 ; APPLICANT: Brenner, Alfred A.  
 ; APPLICANT: Tang, Maria  
 ; APPLICANT: Loper, John C.  
 ; APPLICANT: Gleeson, Martin

; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
 ; TITLE OF INVENTION: P450 OXIDOREDUCTASE  
 ; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF  
 ; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO  
 ; FILE REFERENCE: 1010-16

; CURRENT APPLICATION NUMBER: US/10/139,031  
 ; CURRENT FILING DATE: 2002-05-03  
 ; PRIOR APPLICATION NUMBER: US/09/976,800

; PRIOR FILING DATE: 2001-10-12  
 ; NUMBER OF SEQ ID NOS: 118  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 118  
 ; LENGTH: 679  
 ; TYPE: PRT

; ORGANISM: CANDIDATROPICALIS  
 ; ORGANISM: CANDIDATROPICALIS

US-10-139-031-118

Query Match 0.9%; Score 9; DB 9; Length 679;  
 Best Local Similarity 100.0%; Pred. No. 8;  
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QY 826 PRYSSISS 834  
 Db 437 PRYSSISS 445

RESULT 15

US-10-138-905-83  
 ; Sequence 83, Application US/10138905  
 ; Publication No. US20030068800A1

; GENERAL INFORMATION:  
 ; APPLICANT: Wilson, Ron C.  
 ; APPLICANT: Craft, David L.  
 ; APPLICANT: Eirich, Dudley  
 ; APPLICANT: Eshoo, Mark  
 ; APPLICANT: Madduri, Krishna M.  
 ; APPLICANT: Cornett, Cathy A.  
 ; APPLICANT: Brenner, Alfred A.  
 ; APPLICANT: Tang, Maria  
 ; APPLICANT: Loper, John C.  
 ; APPLICANT: Gleeson, Martin

; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
 ; TITLE OF INVENTION: P450 OXIDOREDUCTASE  
 ; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF  
 ; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO  
 ; FILE REFERENCE: 1010-16

; CURRENT APPLICATION NUMBER: US/10/138,905  
 ; CURRENT FILING DATE: 2002-05-03  
 ; PRIOR APPLICATION NUMBER: US/09/976,800

US-10-138-905-83

; PRIOR FILING DATE: 2001-10-12  
 ; NUMBER OF SEQ ID NOS: 118  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 83  
 ; LENGTH: 679  
 ; TYPE: PRT  
 ; ORGANISM: CANDIDATROPICALIS  
 ; ORGANISM: CANDIDATROPICALIS

US-10-138-905-83

Query Match 0.9%; Score 9; DB 9; Length 679;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSISS 834  
 Db 437 PRYSSISS 445

Search completed: May 29, 2003, 08:40:13  
 Job time : 54 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:28:41 ; Search time 297 Seconds  
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Title: US-10-031-146-2

Perfect score: 1048

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1048	100.0	1048	24	US-10-031-241-35
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4	1048	100.0	1049	1	PCT-US02-11954-2
5	1048	100.0	1049	21	US-09-791-537-53927
6	1048	100.0	1049	24	US-10-031-146-9

7	1048	100.0	1049	25	US-10-125-640-2	Sequence 2, Appli
8	1048	100.0	1049	26	US-10-201-213-2	Sequence 2, Appli
9	846	80.7	1049	22	US-09-856-339A-21	Sequence 21, Appli
10	846	80.7	1049	24	US-10-018-730A-4	Sequence 4, Appli
11	471	44.9	471	21	US-09-791-537-94076	Sequence 94076, A
12	463	44.2	464	1	PCT-US02-11954-3	Sequence 3, Appli
13	463	44.2	464	25	US-10-125-640-3	Sequence 3, Appli
14	458	43.7	458	21	US-09-791-537-116499	Sequence 116499, A
15	455	43.4	455	21	US-09-791-537-8264	Sequence 8264, Ap
16	370	35.3	471	21	US-09-791-537-71271	Sequence 71271, A
17	191	18.2	191	21	US-09-791-537-116501	Sequence 116501, A
18	28	2.7	222	12	US-08-882-163-9	Sequence 9, Appli
19	28	2.7	222	12	US-08-882-163C-9	Sequence 9, Appli
20	28	2.7	1054	1	PCT-US02-11954-5	Sequence 4, Appli
21	28	2.7	1054	1	PCT-US02-11954-5	Sequence 5, Appli
22	28	2.7	1054	21	US-09-791-537-139586	Sequence 139586, A
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26	21	2.0	1061	1	PCT-US02-11954-7	Sequence 7, Appli
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33	16	1.5	659	21	US-09-791-537-71690	Sequence 71690, A
34	16	1.5	659	27	US-60-360-039-2518	Sequence 2518, Ap
35	16	1.5	661	21	US-09-791-537-20730	Sequence 20730, A
36	16	1.5	678	21	US-09-791-537-48331	Sequence 48331, A
37	16	1.5	678	27	US-60-360-039-2517	Sequence 2517, Ap
38	15	1.4	592	27	US-60-360-039-4874	Sequence 4874, Ap
39	15	1.4	592	27	US-60-360-039-7634	Sequence 7634, Ap
40	15	1.4	614	1	PCT-US02-13142-3234	Sequence 3234, Ap
41	15	1.4	614	25	US-10-128-714-3234	Sequence 3234, Ap
42	15	1.4	614	27	US-60-316-362-3234	Sequence 3234, Ap
43	15	1.4	626	18	US-09-417-507-41634	Sequence 41634, A
44	15	1.4	693	21	US-09-791-537-8203	Sequence 8203, Ap
45	15	1.4	693	24	US-10-021-425-38	Sequence 38, Appli

ALIGNMENTS

RESULT 1  
US-10-031-146-2  
; Sequence 2, Application US/100311146  
; GENERAL INFORMATION:  
; APPLICANT: HAUER, Bernhard  
; APPLICANT: PLEISS, Juergen  
; APPLICANT: SCHWANEBERG, Ulrich  
; APPLICANT: SCHMITT, Jutta  
; TITLE OF INVENTION: Novel cytochrome P450 monooxygenases and their use for the ox  
; FILE REFERENCE: 50915  
; CURRENT APPLICATION NUMBER: US/10/031,146  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: PCT/EP 00/07253  
; PRIOR FILING DATE: 2000-07-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Word Perfect version 6.1  
; SEQ ID NO 2  
; LENGTH: 1048  
; TYPE: PRT  
; ORGANISM: Bacillus megaterium  
US-10-031-146-2

Query Match 100.0%; Score 1048; DB 24; Length 1048;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 TIKEMPQKTFGELKNLPLLLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60  
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Db 121 DIAVOLVKWERLNDAHEIEVPDMTRLTLDITGLCGFNRYRNSFYRQPHFFITSMVRA 180  
QY 181 LDEAMNKLQORANPPDPAYDENKROQEDIKVMNDLVDKIIADKASGSGSDLLTHMLNG 240  
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QY 301 PVPSTYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPLQ 360  
Db 301 PVPSTYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPLQ 360  
QY 361 HRDKTIWGDVDEEPRERFENPSPAIPOHAFKPFNGQORACIGQOQFALHEATLVLGMLKH 420  
Db 361 HRDKTIWGDVDEEPRERFENPSPAIPOHAFKPFNGQORACIGQOQFALHEATLVLGMLKH 420  
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QY 541 PDNAKQFVDWLDAQASADEVKGVYRVSFGCGDKNNWATTYQKVPFIDETLAAGAENIADR 600  
Db 541 PDNAKQFVDWLDAQASADEVKGVYRVSFGCGDKNNWATTYQKVPFIDETLAAGAENIADR 600  
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QY 661 AFSNNVASKELQOQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720  
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QY 1021 HOVSADARLWLOLEEKGRYAKOVWAG 1048  
Db 1021 HOVSADARLWLOLEEKGRYAKOVWAG 1048

RESULT 2

US-10-031-241-35

; Sequence 35, Application US/10031241  
; GENERAL INFORMATION:  
; APPLICANT: Hauer, Bernhard  
; APPLICANT: Schmid, Rolf D.  
; APPLICANT: Schwaneberg, Ulrich  
; TITLE OF INVENTION: Electron donor system for enzymes and its use in the biochemic  
; FILE OF INVENTION: conversion of substrates  
; FILE REFERENCE: M/40076  
; CURRENT APPLICATION NUMBER: US/10/031,241  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP00/07251  
; PRIOR FILING DATE: 2000-07-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 1048  
; TYPE: PRT  
; ORGANISM: Bacillus megaterium  
; US-10-031-241-35

Query Match 100.0%; Score 1048; DB 24; Length 1048;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 LDEAMNKLQORANPPDPAYDENKROQEDIKVMNDLVDKIIADKASGSGSDLLTHMLNG 240  
Db 181 LDEAMNKLQORANPPDPAYDENKROQEDIKVMNDLVDKIIADKASGSGSDLLTHMLNG 240  
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Db 481 PLLVLYGSMGTAEGTARDLADIAAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNCHP 540  
QY 541 PDNAKQFVDWLDAQASADEVKGVYRVSFGCGDKNNWATTYQKVPFIDETLAAGAENIADR 600  
Db 541 PDNAKQFVDWLDAQASADEVKGVYRVSFGCGDKNNWATTYQKVPFIDETLAAGAENIADR 600  
QY 601 GEADASDDPEGYEWEHMHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 660  
Db 601 GEADASDDPEGYEWEHMHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 660  
QY 661 AFSNNVASKELQOQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720  
Db 661 AFSNNVASKELQOQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720  
QY 721 DASQQIRLEAEBEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780



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Db 721 DASQIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPHKVEL 780
Qy 781 EALLEKQAYKEQVLAKRLTLMLELKYKACEMKFSFIALLPSPRYSISSPRVDEK 840
Db 781 EALLEKQAYKEQVLAKRLTLMLELKYKACEMKFSFIALLPSPRYSISSPRVDEK 840
Qy 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQSGDITTCFISPPQSEFTLPKDPETPLIM 900
Db 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQSGDITTCFISPPQSEFTLPKDPETPLIM 900
Qy 901 VGPCTGVAPRGVQARKQLKEQOQSLGEAHLFGCRSPHEDLYQBELENAQSEGIITL 960
Db 901 VGPCTGVAPRGVQARKQLKEQOQSLGEAHLFGCRSPHEDLYQBELENAQSEGIITL 960
Qy 961 HTAFSRMPNPKTYVQHVMEQDQKLLIELLDQGAHFYICDGSQMAPAVEATLMKSYADV 1020
Db 961 HTAFSRMPNPKTYVQHVMEQDQKLLIELLDQGAHFYICDGSQMAPAVEATLMKSYADV 1020
Qy 1021 HOYSEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1021 HOYSEADARLWLOOLEEKGRYAKDVWAG 1048

RESULT 3
US-10-031-695-2
; Sequence 2, Application US/10031695
; GENERAL INFORMATION:
; APPLICANT: Hauer, Bernhard
; APPLICANT: Pleiss, Jurgen
; APPLICANT: Schwaneberg, Ulrich
; APPLICANT: Schmitt, Jutta
; TITLE OF INVENTION: Modified cytochrome P450 monooxygenases
; FILE REFERENCE: M/40434
; CURRENT APPLICATION NUMBER: US/10/031,695
; PRIOR FILING DATE: 2002-05-06
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Bacillus megaterium
US-10-031-695-2

Query Match 100.0%; Score 1048; DB 24; Length 1048;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADELGEIPKFEAPGRVTRYLSSQRLIKE 60
Db 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADELGEIPKFEAPGRVTRYLSSQRLIKE 60
Qy 61 ACDESFPDKLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQAMKGYHAMV 120
Db 61 ACDESFPDKLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQAMKGYHAMV 120
Qy 121 DIAVOLVOKERLNADEHIEVPEDMTLTDITGLCGFNFRNSFYRDQPHFITSMVRA 180
Db 121 DIAVOLVOKERLNADEHIEVPEDMTLTDITGLCGFNFRNSFYRDQPHFITSMVRA 180
Qy 181 LDEAMNKLQANPDDPAYDENKRFQFORDIKVMDLVDKIITADKASGEQSDLLTHMLNG 240
Db 181 LDEAMNKLQANPDDPAYDENKRFQFORDIKVMDLVDKIITADKASGEQSDLLTHMLNG 240
Qy 241 KDPETGEPDDEINRQIITFLIAGHETTSGLLSFALYFLVKNPHVQLKAAEEAARVLD 300
Db 241 KDPETGEPDDEINRQIITFLIAGHETTSGLLSFALYFLVKNPHVQLKAAEEAARVLD 300
Qy 301 PVPYSQVKQKLYGVGMVNLALRWPTAPAFSLYAKEDTVLGGEYPLEKDELMVLIPQL 360
Db 301 PVPYSQVKQKLYGVGMVNLALRWPTAPAFSLYAKEDTVLGGEYPLEKDELMVLIPQL 360
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Qy 361 HRDKTIWDDVEFRPERFENPSAIPQHAFFKPGNGORACIGQOQFALHEATVLGMMLKH 420
Db 361 HRDKTIWDDVEFRPERFENPSAIPQHAFFKPGNGORACIGQOQFALHEATVLGMMLKH 420
Qy 421 FDFEDHTNYELDIKETLTLKPEGVVVKAKSKKIPLGIPSPSTEQSAKKYKKAENAHT 480
Db 421 FDFEDHTNYELDIKETLTLKPEGVVVKAKSKKIPLGIPSPSTEQSAKKYKKAENAHT 480
Qy 481 PLLVLGSGNMGTAEGTARDLADTAMSKGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
Db 481 PLLVLGSGNMGTAEGTARDLADTAMSKGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
Qy 541 PDNAKOFVDMLDQASADEVKGVYVFGCGDKKNWATTYQKVPAFIDETLAAKGAENTADR 600
Db 541 PDNAKOFVDMLDQASADEVKGVYVFGCGDKKNWATTYQKVPAFIDETLAAKGAENTADR 600
Qy 601 GEADASDDFEGTYEWEHREHMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPKAKMHG 660
Db 601 GEADASDDFEGTYEWEHREHMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPKAKMHG 660
Qy 661 AFSTNVVASKELQOQPGSARSTRHLELTELKPEASYQEGDHLGVIPRNYEGIVNRTARFGL 720
Db 661 AFSTNVVASKELQOQPGSARSTRHLELTELKPEASYQEGDHLGVIPRNYEGIVNRTARFGL 720
Qy 721 DASQIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPHKVEL 780
Db 721 DASQIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPHKVEL 780
Qy 781 EALLEKQAYKEQVLAKRLTLMLELKYKACEMKFSFIALLPSPRYSISSPRVDEK 840
Db 781 EALLEKQAYKEQVLAKRLTLMLELKYKACEMKFSFIALLPSPRYSISSPRVDEK 840
Qy 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQSGDITTCFISPPQSEFTLPKDPETPLIM 900
Db 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQSGDITTCFISPPQSEFTLPKDPETPLIM 900
Qy 901 VGPCTGVAPRGVQARKQLKEQOQSLGEAHLFGCRSPHEDLYQBELENAQSEGIITL 960
Db 901 VGPCTGVAPRGVQARKQLKEQOQSLGEAHLFGCRSPHEDLYQBELENAQSEGIITL 960
Qy 961 HTAFSRMPNPKTYVQHVMEQDQKLLIELLDQGAHFYICDGSQMAPAVEATLMKSYADV 1020
Db 961 HTAFSRMPNPKTYVQHVMEQDQKLLIELLDQGAHFYICDGSQMAPAVEATLMKSYADV 1020
Qy 1021 HOYSEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1021 HOYSEADARLWLOOLEEKGRYAKDVWAG 1048
```

## RESULT 4

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PCT-US02-11954-2
; Sequence 2, Application PC/TUS0211954
; GENERAL INFORMATION:
; APPLICANT: Cirino, Patrick C.
; APPLICANT: Arnold, Frances H.
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
; FILE REFERENCE: 4058/2K237-W00
; CURRENT APPLICATION NUMBER: PCT/US02/11954
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/284,215
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/288,636
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/340,602
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; PUBLICATION INFORMATION:
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; DATABASE ACCESSION NUMBER: GenBank / P14779  
; DATABASE ENTRY DATE: 1990-04-01  
; RELEVANT RESIDUES: (1)..(1049)  
PCT-US02-11954-2

Query Match 100.0%; Score 1048; DB 1; Length 1049;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKTADDELGEIFKEPGRVTRVYSSORLIKE 60
DB 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKTADDELGEIFKEPGRVTRVYSSORLIKE 61
QY 61 ACDESFRDKNLSQALKFYRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAKMGYHAMV 120
DB 61 ACDESFRDKNLSQALKFYRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAKMGYHAMV 121
QY 121 DIAVOLQVWERLNDAHEIEVPEDMTRLTLDIGLCGFNYRNSFYRDPHPFITSMVRA 180
DB 121 DIAVOLQVWERLNDAHEIEVPEDMTRLTLDIGLCGFNYRNSFYRDPHPFITSMVRA 181
QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEOSDILLTHMLNG 240
DB 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEOSDILLTHMLNG 241
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEEAARVLD 300
DB 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEEAARVLD 301
QY 301 PVPSTKQVQKLYGVNVLNEALRLWPTAPAFSLYAKEDTVLGGEPLEKGDDELVLIPOL 360
DB 301 PVPSTKQVQKLYGVNVLNEALRLWPTAPAFSLYAKEDTVLGGEPLEKGDDELVLIPOL 361
QY 361 HRDKTIWGDVVEEFPREFENPSAIPQHAFKPFNGQORACIGQOAFALHEATLVGLMKLKH 420
DB 361 HRDKTIWGDVVEEFPREFENPSAIPQHAFKPFNGQORACIGQOAFALHEATLVGLMKLKH 421
QY 421 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKKIPLGGIPSPSTEOSAKVRKKAENAHNT 480
DB 421 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKKIPLGGIPSPSTEOSAKVRKKAENAHNT 481
QY 481 PLLVLYGSMNGTAECTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIYTSVNGHP 540
DB 481 PLLVLYGSMNGTAECTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIYTSVNGHP 541
QY 541 PDNAKQFVDWLDOASADEVKGVYRVSFGCGDNWATTYQKVPFIDETLAAGAENIADR 600
DB 541 PDNAKQFVDWLDOASADEVKGVYRVSFGCGDNWATTYQKVPFIDETLAAGAENIADR 601
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QY 961 HTAFSRMPNQPKTYVQHVMEQDGKGLIELLDQGAHFYICGDSQSNAPAVEATLMKSYADV 1020
DB 962 HTAFSRMPNQPKTYVQHVMEQDGKGLIELLDQGAHFYICGDSQSNAPAVEATLMKSYADV 1021
QY 1021 HOVSADARLWLOOLEEKGRYAKDWAG 1048
DB 1022 HOVSADARLWLOOLEEKGRYAKDWAG 1049
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## RESULT 5

US-09-791-537-53927

; Sequence 53927, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Dancer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09791,537

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 53927

; LENGTH: 1049

; TYPE: PRT

; ORGANISM: Bacillus megaterium

; US-09-791-537-53927

Query Match 100.0%; Score 1048; DB 21; Length 1049;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKTADDELGEIFKEPGRVTRVYSSORLIKE 60
DB 2 TIKEMPOKTFGELKNLPLNTDKPVQALMKTADDELGEIFKEPGRVTRVYSSORLIKE 61
QY 61 ACDESFRDKNLSQALKFYRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAKMGYHAMV 120
DB 62 ACDESFRDKNLSQALKFYRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAKMGYHAMV 121
QY 121 DIAVOLQVWERLNDAHEIEVPEDMTRLTLDIGLCGFNYRNSFYRDPHPFITSMVRA 180
DB 122 DIAVOLQVWERLNDAHEIEVPEDMTRLTLDIGLCGFNYRNSFYRDPHPFITSMVRA 181
QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEOSDILLTHMLNG 240
DB 182 LDEAMNKLQANPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEOSDILLTHMLNG 241
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEEAARVLD 300
DB 242 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEEAARVLD 301
QY 301 PVPSTKQVQKLYGVNVLNEALRLWPTAPAFSLYAKEDTVLGGEPLEKGDDELVLIPOL 360
DB 302 PVPSTKQVQKLYGVNVLNEALRLWPTAPAFSLYAKEDTVLGGEPLEKGDDELVLIPOL 361
QY 361 HRDKTIWGDVVEEFPREFENPSAIPQHAFKPFNGQORACIGQOAFALHEATLVGLMKLKH 420
DB 362 HRDKTIWGDVVEEFPREFENPSAIPQHAFKPFNGQORACIGQOAFALHEATLVGLMKLKH 421
QY 421 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKKIPLGGIPSPSTEOSAKVRKKAENAHNT 480
DB 422 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKKIPLGGIPSPSTEOSAKVRKKAENAHNT 481
QY 481 PLLVLYGSMNGTAECTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIYTSVNGHP 540
DB 482 PLLVLYGSMNGTAECTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIYTSVNGHP 541
QY 541 PDNAKQFVDWLDOASADEVKGVYRVSFGCGDNWATTYQKVPFIDETLAAGAENIADR 600
DB 542 PDNAKQFVDWLDOASADEVKGVYRVSFGCGDNWATTYQKVPFIDETLAAGAENIADR 601
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QY 601 GEADASDDDEGTYYEWRHMSDVAAYFNLDIENSDNKSTLSLOFVDSAADPLAKMHG 660
Db 602 GEADASDDDEGTYYEWRHMSDVAAYFNLDIENSDNKSTLSLOFVDSAADPLAKMHG 661
QY 661 AFTSTNVVSKELQOQPGSARSTRHLETELPEKASYQEGDHLGVIPRNYEGIVNRVTARFGL 720
Db 662 AFTSTNVVSKELQOQPGSARSTRHLETELPEKASYQEGDHLGVIPRNYEGIVNRVTARFGL 721
QY 721 DASQQIRLAEAEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Db 722 DASQQIRLAEAEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781
QY 781 EALLERQAYKEQVLAKRLTLMLELEKYPACEMKFSEFIALPSIRPRYYSISSSPRVDEK 840
Db 782 EALLERQAYKEQVLAKRLTLMLELEKYPACEMKFSEFIALPSIRPRYYSISSSPRVDEK 841
QY 841 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDITICFISTPQSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDITICFISTPQSEFTLPKDPETPLIM 901
QY 901 VGPCTGVAPFRGVQARKQLKEQGQSLGEAHLFGCRSPHEDYLYQEELNAQSEGIITL 960
Db 902 VGPCTGVAPFRGVQARKQLKEQGQSLGEAHLFGCRSPHEDYLYQEELNAQSEGIITL 961
QY 961 HTAFSRMPNPKTYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 962 HTAFSRMPNPKTYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021
QY 1021 HQVSEADARLWQLEEKGRYAKDVWAG 1048
Db 1022 HQVSEADARLWQLEEKGRYAKDVWAG 1049
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## RESULT 6

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US-10-031-146-9
; Sequence 9, Application US/10031146
; GENERAL INFORMATION:
; APPLICANT: HAUER, Bernhard
; APPLICANT: PLEISS, Juergen
; APPLICANT: SCHWANEBERG, Ulrich
; APPLICANT: SCHMITT, Jutta
; TITLE OF INVENTION: Novel cytochrome P450 monooxygenases and their use for the oxidation
; FILE REFERENCE: 50915
; CURRENT APPLICATION NUMBER: US/10/031,146
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/EP 00/07253
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Word Perfect version 6.1
; SEQ ID NO 9
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
US-10-031-146-9
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Query Match 100.0%; Score 1048; DB 24; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TIKEMPQKTFGELKKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60
Db 2 TIKEMPQKTFGELKKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 61
QY 61 ACDESFRDKNLSQALFVRDFAGDGLFTSWTHKEKNKKAHNILLPFSQOAMGYHAMV 120
Db 62 ACDESFRDKNLSQALFVRDFAGDGLFTSWTHKEKNKKAHNILLPFSQOAMGYHAMV 121
QY 121 DIAVOLQVQWRNLNADHEIPEVDMTRLTLDITGLCGFNRYRNSFYRQDPHPFITMSWRA 180
Db 122 DIAVOLQVQWRNLNADHEIPEVDMTRLTLDITGLCGFNRYRNSFYRQDPHPFITMSWRA 181
QY 181 LDEAMNKLQRPDDPAYDENKRFQEDIKVMDLVDKIIADRKAQSGESDDLLTHMLNG 240
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Db 182 LDEAMNKLQRPDDPAYDENKRFQEDIKVMDLVDKIIADRKAQSGESDDLLTHMLNG 241
QY 241 KPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVD 300
Db 242 KPETGEPLDDENIRYQIIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVD 301
QY 301 PVPYSYQVQKQKLVGMVNLNEALRLWPTAPAFSYAKEDTVLGGEYPLEKGEDELWVLIPOL 360
Db 302 PVPYSYQVQKQKLVGMVNLNEALRLWPTAPAFSYAKEDTVLGGEYPLEKGEDELWVLIPOL 361
QY 361 HRDKTIWGDVVEFRPERFENPSAIPQHAFKPPGNGQRACIGQOFALHEATVLGMLMKH 420
Db 362 HRDKTIWGDVVEFRPERFENPSAIPQHAFKPPGNGQRACIGQOFALHEATVLGMLMKH 421
QY 421 FQFEDHTNYELDIKETLTLKPEGFVVYKAKSKKIPLGIGIPSPSTEQSAKKVKKAEANHT 480
Db 422 FQFEDHTNYELDIKETLTLKPEGFVVYKAKSKKIPLGIGIPSPSTEQSAKKVKKAEANHT 481
QY 481 PLILVLYGSNNGTAEGTARDLADIAMSGKGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
Db 482 PLILVLYGSNNGTAEGTARDLADIAMSGKGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 541
QY 541 PDNAKQFVDWLQDQASADEVKGVRYSVFGCGDKKNWATTYQKVPAFIDETTLAAGAENIADR 600
Db 542 PDNAKQFVDWLQDQASADEVKGVRYSVFGCGDKKNWATTYQKVPAFIDETTLAAGAENIADR 601
QY 601 GEADASDDDEGTYYEWRHMSDVAAYFNLDIENSDNKSTLSLOFVDSAADPLAKMHG 660
Db 602 GEADASDDDEGTYYEWRHMSDVAAYFNLDIENSDNKSTLSLOFVDSAADPLAKMHG 661
QY 661 AFTSTNVVSKELQOQPGSARSTRHLETELPEKASYQEGDHLGVIPRNYEGIVNRVTARFGL 720
Db 662 AFTSTNVVSKELQOQPGSARSTRHLETELPEKASYQEGDHLGVIPRNYEGIVNRVTARFGL 721
QY 721 DASQQIRLAEAEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
Db 722 DASQQIRLAEAEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781
QY 781 EALLERQAYKEQVLAKRLTLMLELEKYPACEMKFSEFIALPSIRPRYYSISSSPRVDEK 840
Db 782 EALLERQAYKEQVLAKRLTLMLELEKYPACEMKFSEFIALPSIRPRYYSISSSPRVDEK 841
QY 841 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDITICFISTPQSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDITICFISTPQSEFTLPKDPETPLIM 901
QY 901 VGPCTGVAPFRGVQARKQLKEQGQSLGEAHLFGCRSPHEDYLYQEELNAQSEGIITL 960
Db 902 VGPCTGVAPFRGVQARKQLKEQGQSLGEAHLFGCRSPHEDYLYQEELNAQSEGIITL 961
QY 961 HTAFSRMPNPKTYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 962 HTAFSRMPNPKTYVQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021
QY 1021 HQVSEADARLWQLEEKGRYAKDVWAG 1048
Db 1022 HQVSEADARLWQLEEKGRYAKDVWAG 1049
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## RESULT 7

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US-10-125-640-2
; Sequence 2, Application US/10125640
; GENERAL INFORMATION:
; APPLICANT: Cirino, Patrick C.
; APPLICANT: Arnold, Frances H.
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
; FILE REFERENCE: 4058/1K237-US3
; CURRENT APPLICATION NUMBER: US/10/125,640
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/284,215
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/288,636
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; PRIOR FILING DATE: 2001-05-03  
 ; PRIOR APPLICATION NUMBER: 60/340,602  
 ; PRIOR FILING DATE: 2001-12-12  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 1049  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus megaterium  
 ; PUBLIC INFORMATION:  
 ; DATABASE ACCESSION NUMBER: GenBank / P14779  
 ; DATABASE ENTRY DATE: 1990-04-01  
 ; RELEVANT RESIDUES: (1)..(1049)  
 US-10-125-640-2

Query Match 100.0%; Score 1048; DB 25; Length 1049;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TIKEMPOKTFGELKNLPLNTDKPQALMKIADDELGEIFKEPGRVTRYLSSORLIKE	60
DB	2	TIKEMPOKTFGELKNLPLNTDKPQALMKIADDELGEIFKEPGRVTRYLSSORLIKE	61
QY	61	ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	120
DB	62	ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	121
QY	121	DIAVOLVKWERLNDAHEIEVPEDMTLTDITGLCGFNYSFYRDPHFITSMVRA	180
DB	122	DIAVOLVKWERLNDAHEIEVPEDMTLTDITGLCGFNYSFYRDPHFITSMVRA	181
QY	181	LDEAMNKLRANPPDPAYDENKRFQEDIKVNDLVDKIIADRKASGESQDOLLTHMLNG	240
DB	182	LDEAMNKLRANPPDPAYDENKRFQEDIKVNDLVDKIIADRKASGESQDOLLTHMLNG	241
QY	241	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD	300
DB	242	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD	301
QY	301	PVPYSKQVKQLYGVNVLNEALRLWPTAPAFSLYAKEDTVLGGEPLEKGDLMVLIPOL	360
DB	302	PVPYSKQVKQLYGVNVLNEALRLWPTAPAFSLYAKEDTVLGGEPLEKGDLMVLIPOL	361
QY	361	HRDKTIWGDVVEFRPERENPFAIPQHAFFKPGNGQACICQOQFALHEATLVLMKXK	420
DB	362	HRDKTIWGDVVEFRPERENPFAIPQHAFFKPGNGQACICQOQFALHEATLVLMKXK	421
QY	421	DFEDHTNYELDIKETLTKPGEFVVKAKSKKIPILGGIPSPSTEQSAKKVRKAENAHNT	480
DB	422	DFEDHTNYELDIKETLTKPGEFVVKAKSKKIPILGGIPSPSTEQSAKKVRKAENAHNT	481
QY	481	PLLVLYGSMGTAEGRDADLADIAKSGFAPQVATLDHAGNLPREGAVLIIVTASVNGHP	540
DB	482	PLLVLYGSMGTAEGRDADLADIAKSGFAPQVATLDHAGNLPREGAVLIIVTASVNGHP	541
QY	541	PONAKQFVWLDOASADEVKGVRYSVFGCGDKNWTATYQKVPFIDETLAAGAENIADR	600
DB	542	PONAKQFVWLDOASADEVKGVRYSVFGCGDKNWTATYQKVPFIDETLAAGAENIADR	601
QY	601	GEADASDDPEGTYEWEHMHWSVAAVFNLDITENSEDNKSTLSLQFVDSAADMPKAKHG	660
DB	602	GEADASDDPEGTYEWEHMHWSVAAVFNLDITENSEDNKSTLSLQFVDSAADMPKAKHG	661
QY	661	AFSTNVVASKELQPGSARSTRHLELPKEASYOEGDHLGVIIPRNYEGIVNRVTRFGL	720
DB	662	AFSTNVVASKELQPGSARSTRHLELPKEASYOEGDHLGVIIPRNYEGIVNRVTRFGL	721
QY	721	DASQQLRLAEAEKLAHLPLAKTVSVEELQYVLEQDPVTRTQLRAMAAKTVCPPHKVEL	780
DB	722	DASQQLRLAEAEKLAHLPLAKTVSVEELQYVLEQDPVTRTQLRAMAAKTVCPPHKVEL	781
QY	781	EALLEKQAKQVLAQKRLTLMLELLEKYPACEMKSEFFALLPSIRPRYSSISSPRVDEK	840

DB	782	EALLEKQAKQVLAQKRLTLMLELLEKYPACEMKSEFFALLPSIRPRYSSISSPRVDEK	841
QY	841	QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIM	900
DB	842	QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIM	901
QY	901	VGPGTGVAPFRGFGVQARKQKQEGOSLGEAHLYFCRSPHEDYLYQEELNAQSEGIITL	960
DB	902	VGPGTGVAPFRGFGVQARKQKQEGOSLGEAHLYFCRSPHEDYLYQEELNAQSEGIITL	961
QY	961	HTAFSRMPNQPKTYVQHVMEQDGKLLIELLDQGAHFYICGDSQSOMAPAVEATLMKSYAD	1020
DB	962	HTAFSRMPNQPKTYVQHVMEQDGKLLIELLDQGAHFYICGDSQSOMAPAVEATLMKSYAD	1021
QY	1021	HOVSADARLWLQOLEEKGRYAKDYWAG	1048
DB	1022	HOVSADARLWLQOLEEKGRYAKDYWAG	1049

RESULT 8  
 US-10-201-213-2  
 ; Sequence 2, Application US/10201213  
 ; GENERAL INFORMATION:  
 ; APPLICANT: California Institute of Technology  
 ; APPLICANT: Farinas, Edgardo  
 ; APPLICANT: Glieder, Anton  
 ; APPLICANT: Arnold, Frances  
 ; APPLICANT: Schwanberg, Ulrich  
 ; TITLE OF INVENTION: IMPROVED CYTOCHROME P450 OXYGENASES  
 ; FILE REFERENCE: 3369/IK238-US2  
 ; CURRENT APPLICATION NUMBER: US/10/201,213  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: US 60/306,766  
 ; PRIOR FILING DATE: 2001-07-20  
 ; PRIOR APPLICATION NUMBER: US 60/308,429  
 ; PRIOR FILING DATE: 2001-07-27  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 1049  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus megaterium  
 ; PUBLIC INFORMATION:  
 ; DATABASE ACCESSION NUMBER: GenBank / P14779  
 ; DATABASE ENTRY DATE: 1990-04-01  
 ; RELEVANT RESIDUES: (1)..(1049)  
 US-10-201-213-2

Query Match 100.0%; Score 1048; DB 26; Length 1049;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TIKEMPOKTFGELKNLPLNTDKPQALMKIADDELGEIFKEPGRVTRYLSSORLIKE	60
DB	2	TIKEMPOKTFGELKNLPLNTDKPQALMKIADDELGEIFKEPGRVTRYLSSORLIKE	61
QY	61	ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	120
DB	62	ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	121
QY	121	DIAVOLVKWERLNDAHEIEVPEDMTLTDITGLCGFNYSFYRDPHFITSMVRA	180
DB	122	DIAVOLVKWERLNDAHEIEVPEDMTLTDITGLCGFNYSFYRDPHFITSMVRA	181
QY	181	LDEAMNKLRANPPDPAYDENKRFQEDIKVNDLVDKIIADRKASGESQDOLLTHMLNG	240
DB	182	LDEAMNKLRANPPDPAYDENKRFQEDIKVNDLVDKIIADRKASGESQDOLLTHMLNG	241
QY	241	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD	300
DB	242	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD	301
QY	301	PVPYSKQVKQLYGVNVLNEALRLWPTAPAFSLYAKEDTVLGGEPLEKGDLMVLIPOL	360

Db 302 PVPSTYQVKQKLVGVNLEALWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLPQL 361  
QY 361 HRDKTWGGDVEEFRRPERFENPSAIPQHAEPKPGNGORACIGQGFALHEATLVLGWMLKH 420  
Db 362 HRDKTWGGDVEEFRRPERFENPSAIPQHAEPKPGNGORACIGQGFALHEATLVLGWMLKH 421  
QY 421 DFEEDHTNYELDIKETITLKPGEFVVKAKSKKIPLAGIPSPSTEQSAKKVKKKAENAHNT 480  
Db 422 DFEEDHTNYELDIKETITLKPGEFVVKAKSKKIPLAGIPSPSTEQSAKKVKKKAENAHNT 481  
QY 481 PLVLVYSGNMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540  
Db 482 PLVLVYSGNMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 541  
QY 541 PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWTYYQKVPFIDETLAAGAENIADR 600  
Db 542 PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWTYYQKVPFIDETLAAGAENIADR 601  
QY 601 GEADASDDFEGTYEENREHMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMP LAKMHG 660  
Db 602 GEADASDDFEGTYEENREHMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMP LAKMHG 661  
QY 661 AFSTNVVASKELQOPGSARSTRHLEIPELPEASVQEGDHLGVIPRNYEGIVNRTARFGL 720  
Db 662 AFSTNVVASKELQOPGSARSTRHLEIPELPEASVQEGDHLGVIPRNYEGIVNRTARFGL 721  
QY 721 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQIRAMAATVCPPHKVEL 780  
Db 722 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQIRAMAATVCPPHKVEL 781  
QY 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKFSEFIALPSIRPRYISSSPRYDEK 840  
Db 782 EALLEKQAYKEQVLAKRLTMELEKYPACEMKFSEFIALPSIRPRYISSSPRYDEK 841  
QY 841 QASITVSVSGEAWSGYGKYGTASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900  
Db 842 QASITVSVSGEAWSGYGKYGTASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 901  
QY 901 VGPCTGVAPRGFVQARKQLKEQOSLGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 960  
Db 902 VGPCTGVAPRGFVQARKQLKEQOSLGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 961

## RESULT 9

US-09-856-339A-21  
; Sequence 21, Application US/09856339A  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Luet  
; APPLICANT: Bell, Stephen  
; APPLICANT: Carmichael, Angus  
; TITLE OF INVENTION: PROCESS FOR OXIDISING TERPENES  
; FILE REFERENCE: HO-P02196USO (10104571)  
; CURRENT APPLICATION NUMBER: US/09/856,339A  
; CURRENT FILING DATE: 2001-05-18  
; PRIOR FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: GB 9825421.2  
; PRIOR FILING DATE: 1998-11-19  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 21  
; LENGTH: 1049  
; TYPE: PRT  
; ORGANISM: Bacillus megaterium

FEATURE:  
; NAME/KEY: MUTAGEN  
; LOCATION: (1)..(1049)  
; OTHER INFORMATION: Coding sequence  
US-09-856-339A-21  
  
Query Match 80.7%; Score 846; DB 22; Length 1049;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 TIKEMPQPKTFGELKNPLPILNTPKPVQALMKIADELGEIFKFEAPGRVTRYLLSQRLIKE 60  
Db 2 TIKEMPQPKTFGELKNPLPILNTPKPVQALMKIADELGEIFKFEAPGRVTRYLLSQRLIKE 61  
QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAKMKYHAMV 120  
Db 62 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAKMKYHAMV 121  
QY 121 DIAVOLVQVKWERLNADSHIEVPEDMTRLTLDITGLCGFNRYRNSFYRDQPHPTTSMVRA 180  
Db 122 DIAVOLVQVKWERLNADSHIEVPEDMTRLTLDITGLCGFNRYRNSFYRDQPHPTTSMVRA 181  
QY 181 LDEAMNKLQANPDDPAYDENKQFOEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 240  
Db 182 LDEAMNKLQANPDDPAYDENKQFOEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 241  
QY 241 KDPETGEPLDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLD 300  
Db 242 KDPETGEPLDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLD 301  
QY 301 PVPSTYQVKQKLVGVNLEALWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLPQL 360  
Db 302 PVPSTYQVKQKLVGVNLEALWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLPQL 361  
QY 361 HRDKTWGGDVEEFRRPERFENPSAIPQHAEPKPGNGORACIGQGFALHEATLVLGWMLKH 420  
Db 362 HRDKTWGGDVEEFRRPERFENPSAIPQHAEPKPGNGORACIGQGFALHEATLVLGWMLKH 421  
QY 421 DFEEDHTNYELDIKETITLKPGEFVVKAKSKKIPLAGIPSPSTEQSAKKVKKKAENAHNT 480  
Db 422 DFEEDHTNYELDIKETITLKPGEFVVKAKSKKIPLAGIPSPSTEQSAKKVKKKAENAHNT 481  
QY 481 PLVLVYSGNMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540  
Db 482 PLVLVYSGNMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 541  
QY 541 PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWTYYQKVPFIDETLAAGAENIADR 600  
Db 542 PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWTYYQKVPFIDETLAAGAENIADR 601  
QY 601 GEADASDDFEGTYEENREHMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMP LAKMHG 660  
Db 602 GEADASDDFEGTYEENREHMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADMP LAKMHG 661  
QY 661 AFSTNVVASKELQOPGSARSTRHLEIPELPEASVQEGDHLGVIPRNYEGIVNRTARFGL 720  
Db 662 AFSTNVVASKELQOPGSARSTRHLEIPELPEASVQEGDHLGVIPRNYEGIVNRTARFGL 721  
QY 721 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQIRAMAATVCPPHKVEL 780  
Db 722 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQIRAMAATVCPPHKVEL 781  
QY 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKFSEFIALPSIRPRYISSSPRYDEK 840  
Db 782 EALLEKQAYKEQVLAKRLTMELEKYPACEMKFSEFIALPSIRPRYISSSPRYDEK 841  
QY 841 QASITVSVSGEAWSGYGKYGTASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900  
Db 842 QASITVSVSGEAWSGYGKYGTASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 901  
QY 901 VGPCTGVAPRGFVQARKQLKEQOSLGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 960  
Db 902 VGPCTGVAPRGFVQARKQLKEQOSLGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 961

QY 961 HTAFSRMPNPKTYVQHVMEQDGKKLIELLDGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 DB 962 HTAFSRMPNPKTYVQHVMEQDGKKLIELLDGAHFYICGDSQMAPAVEATLMKSYADV 1021  
 QY 1021 HQVSEADARLWLQOLEEKGRYAKDVWAG 1048  
 DB 1022 HQVSEADARLWLQOLEEKGRYAKDVWAG 1049

RESULT 10  
 US-10-018-730A-4  
 ; Sequence 4, Application US/10018730A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Luet, Wong  
 ; APPLICANT: Jonathap, Jones  
 ; TITLE OF INVENTION: PROCESS FOR OXIDISING AROMATIC COMPOUNDS  
 ; FILE REFERENCE: P02353051 / 10112404 / N.76277B  
 ; CURRENT APPLICATION NUMBER: US/10/018,730A  
 ; CURRENT FILING DATE: 2002-04-04  
 ; PRIOR APPLICATION NUMBER: GB 9914373.7  
 ; PRIOR FILING DATE: 1999-06-18  
 ; PRIOR APPLICATION NUMBER: PCT/GB00/02379  
 ; PRIOR FILING DATE: 2000-06-19  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 1049  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus megaterium  
 US-10-018-730A-4

Query Match 80.7%; Score 846; DB 24; Length 1049;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60  
 DB 2 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 61  
 QY 61 ACDESFRDNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQOAMKGYHAMV 120  
 DB 62 ACDESFRDNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQOAMKGYHAMV 121  
 QY 121 DIAVOLQKWERLNADEHIEVPEDMTRLTDLTIGLCGFNYRNSFYRQDPHFITSVMRA 180  
 DB 122 DIAVOLQKWERLNADEHIEVPEDMTRLTDLTIGLCGFNYRNSFYRQDPHFITSVMRA 181  
 QY 181 LDEAMNKLQANPPDPAYDENKRFQEDIKVMNDLVKIIADRKASGESQSDLLTHMLNG 240  
 DB 182 LDEAMNKLQANPPDPAYDENKRFQEDIKVMNDLVKIIADRKASGESQSDLLTHMLNG 241  
 QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYELVKNPHVLOKAAEAAARVLD 300  
 DB 242 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYELVKNPHVLOKAAEAAARVLD 301  
 QY 301 PVPYSQVQKQKYGVNVLNEALRLMPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPL 360  
 DB 302 PAPSQVQKQKYGVNVLNEALRLMPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPL 361  
 QY 361 HRDKTIWGDVVEEPRERENFSAIPQAFKPFNGORACICQOQFALHEATLVLMMLKH 420  
 DB 362 HRDKTIWGDVVEEPRERENFSAIPQAFKPFNGORACICQOQFALHEATLVLMMLKH 421  
 QY 421 FPFEDHTNYELDIKETLTLPKPGFVYVAKSKKIPGGIPSPSTEOSAKKVRKKAENAHNT 480  
 DB 422 FPFEDHTNYELDIKETLTLPKPGFVYVAKSKKIPGGIPSPSTEOSAKKVRKKAENAHNT 481  
 QY 481 PLLVLGYSNMGTAEGRDADLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASYNCHP 540  
 DB 482 PLLVLGYSNMGTAEGRDADLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASYNCHP 541  
 QY 541 PDNAKQFVDWLQASADEVKGVYRVSFGCGDKNWTYQKVPAFIDETLAAGAENIADR 600

DB 542 PDNAKQFVDWLQASADEVKGVYRVSFGCGDKNWTYQKVPAFIDETLAAGAENIADR 601  
 QY 601 GEADASDDFEGTYEWEHMHWSVAAAYFNLDITENSEDNKSTLSLQFVDSAADMPKAMHG 660  
 DB 602 GEADASDDFEGTYEWEHMHWSVAAAYFNLDITENSEDNKSTLSLQFVDSAADMPKAMHG 661  
 QY 661 AFTSNVASKELQOPGCSARSTRHLEIETLPKEASYEGDHLGVIIPRYEGIVNRVTRARFGL 720  
 DB 662 AFTSNVASKELQOPGCSARSTRHLEIETLPKEASYEGDHLGVIIPRYEGIVNRVTRARFGL 721  
 QY 721 DASQOIRLEAEKEELAHPLAKTVSVEELQVVELQDPVTRTQLRAMAATVCPPHKVEL 780  
 DB 722 DASQOIRLEAEKEELAHPLAKTVSVEELQVVELQDPVTRTQLRAMAATVCPPHKVEL 781  
 QY 781 EALLEKQAYKEOVLAKRLTLMLELLEKYPACEMKFEFIALLSIRPRYYSISSPRVDEK 840  
 DB 782 EALLEKQAYKEOVLAKRLTLMLELLEKYPACEMKFEFIALLSIRPRYYSISSPRVDEK 841  
 QY 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900  
 DB 842 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 901  
 QY 901 VGPGTGVAPFRGFGVQARKQKQEGOSLGEAHLYFCGRSPHEDYLYOELENAQSEGIITL 960  
 DB 902 VGPGTGVAPFRGFGVQARKQKQEGOSLGEAHLYFCGRSPHEDYLYOELENAQSEGIITL 961  
 QY 961 HTAFSRMPNPKTYVQHVMEQDGKKLIELLDGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 DB 962 HTAFSRMPNPKTYVQHVMEQDGKKLIELLDGAHFYICGDSQMAPAVEATLMKSYADV 1021  
 QY 1021 HQVSEADARLWLQOLEEKGRYAKDVWAG 1048  
 DB 1022 HQVSEADARLWLQOLEEKGRYAKDVWAG 1049

RESULT 11  
 US-09-791-537-94076  
 ; Sequence 94076, Application US/09791537  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bloncomix, Inc.  
 ; APPLICANT: Debe, Derek  
 ; APPLICANT: Dancer, Joseph  
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
 ; FILE REFERENCE: 261/210  
 ; CURRENT APPLICATION NUMBER: US/09/791,537  
 ; CURRENT FILING DATE: 2001-02-22  
 ; NUMBER OF SEQ ID NOS: 153055  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 94076  
 ; LENGTH: 471  
 ; TYPE: PRT  
 ; ORGANISM: pdb 2HPDA  
 US-09-791-537-94076

Query Match 44.9%; Score 471; DB 21; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60  
 DB 1 TIKEMPOKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60  
 QY 61 ACDESFRDNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQOAMKGYHAMV 120  
 DB 61 ACDESFRDNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQOAMKGYHAMV 120  
 QY 121 DIAVOLQKWERLNADEHIEVPEDMTRLTDLTIGLCGFNYRNSFYRQDPHFITSVMRA 180  
 DB 121 DIAVOLQKWERLNADEHIEVPEDMTRLTDLTIGLCGFNYRNSFYRQDPHFITSVMRA 180  
 QY 181 LDEAMNKLQANPPDPAYDENKRFQEDIKVMNDLVKIIADRKASGESQSDLLTHMLNG 240

```

181 LDEAMNKLQANPDPPAYDENKRFQEDIKVMDLVDKIADRKASQSDLLTHMLG 240
241 KDPETGPELDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARLVD 300
241 KDPETGPELDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARLVD 300
301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSPFNGQORACIGQGFALHEATLVLGMLKH 360
301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSPFNGQORACIGQGFALHEATLVLGMLKH 360
361 HRDKTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 420
361 HRDKTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 420
421 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPSTEQSAKKVR 471
421 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPSTEQSAKKVR 471

RESULT 12
PCT-US02-11954-3
; Sequence 3, Application PC/TUS0211954
; GENERAL INFORMATION:
; APPLICANT: Cirino, Patrick C.
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
; FILE REFERENCE: 4058/2K237-WO
; CURRENT APPLICATION NUMBER: PCT/US02/11954
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/284,215
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/288,636
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/340,602
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank / P14779
; DATABASE ENTRY DATE: 1990-04-01
; RELEVANT RESIDUES: (1)..(464)
PCT-US02-11954-3

Query Match 44.2%; Score 463; DB 1; Length 464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGELKNPLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60
Db 2 TIKEMPOKTFGELKNPLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 61
61 ACDESREFDKNLQALKFVRDPAGDGLFTSWTHKNWKAHNILLPSFSQQAAMGYHAMV 120
62 ACDESREFDKNLQALKFVRDPAGDGLFTSWTHKNWKAHNILLPSFSQQAAMGYHAMV 121
121 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDITGLCGFNFRNFSYRQDPHPFITSMVRA 180
122 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDITGLCGFNFRNFSYRQDPHPFITSMVRA 181
181 LDEAMNKLQANPDPPAYDENKRFQEDIKVMDLVDKIADRKASQSDLLTHMLG 240
182 LDEAMNKLQANPDPPAYDENKRFQEDIKVMDLVDKIADRKASQSDLLTHMLG 241
241 KDPETGPELDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARLVD 300
242 KDPETGPELDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARLVD 301
301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSPFNGQORACIGQGFALHEATLVLGMLKH 420
301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSPFNGQORACIGQGFALHEATLVLGMLKH 420
361 HRDKTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 480
361 HRDKTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 480
421 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPSTEQSAKKVR 463
421 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPSTEQSAKKVR 463
```

```

302 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 361
361 HRDKTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 420
362 HRDKTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 421
421 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPST 463
422 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPST 464

RESULT 13
US-10-125-640-3
; Sequence 3, Application US/10125640
; GENERAL INFORMATION:
; APPLICANT: Cirino, Patrick C.
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
; FILE REFERENCE: 4058/1K237-US3
; CURRENT APPLICATION NUMBER: US/10/125,640
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/284,215
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/288,636
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/340,602
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Bacillus megaterium
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank / P14779
; DATABASE ENTRY DATE: 1990-04-01
; RELEVANT RESIDUES: (1)..(464)
US-10-125-640-3

Query Match 44.2%; Score 463; DB 25; Length 464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGELKNPLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 60
Db 2 TIKEMPOKTFGELKNPLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSORLIKE 61
61 ACDESREFDKNLQALKFVRDPAGDGLFTSWTHKNWKAHNILLPSFSQQAAMGYHAMV 120
62 ACDESREFDKNLQALKFVRDPAGDGLFTSWTHKNWKAHNILLPSFSQQAAMGYHAMV 121
121 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDITGLCGFNFRNFSYRQDPHPFITSMVRA 180
122 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDITGLCGFNFRNFSYRQDPHPFITSMVRA 181
181 LDEAMNKLQANPDPPAYDENKRFQEDIKVMDLVDKIADRKASQSDLLTHMLG 240
182 LDEAMNKLQANPDPPAYDENKRFQEDIKVMDLVDKIADRKASQSDLLTHMLG 241
241 KDPETGPELDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARLVD 300
242 KDPETGPELDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARLVD 301
301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 360
302 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDLMVLIPQL 361
361 HRDKTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 420
362 HRDKTINGDDVEEPRPERFENPSAIPQHAFFKPFNGQORACIGQGFALHEATLVLGMLKH 421
421 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPST 463
421 FDFEDHTNYELDIKETITLTKPEGFVWRAKSKKIPLGIPSPST 463
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|||||  
Db 422 FDFEDHTNYELDIKETLTLLKPEGVYVKAQSKKIPLGGIPSPST 454

## RESULT 14

US-09-791-537-116499  
; Sequence 116499, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 116499  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: pdb 1B1YA  
US-09-791-537-116499

Query Match 43.7%; Score 458; DB 21; Length 458;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPQKTFGELKKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60  
|||||  
Db 1 TIKEMPQKTFGELKKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60  
|||||  
QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 120  
|||||  
Db 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 120  
|||||  
QY 121 DIAVOLVQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNRYNSFYRDQPHFITSWVRA 180  
|||||  
Db 121 DIAVOLVQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNRYNSFYRDQPHFITSWVRA 180  
|||||  
QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG 240  
|||||  
Db 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG 240  
|||||  
QY 241 KPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVQLQAAEAAARVLD 300  
|||||  
Db 241 KPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVQLQAAEAAARVLD 300  
|||||  
QY 301 PVPYSYQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELMLVLPOL 360  
|||||  
Db 301 PVPYSYQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELMLVLPOL 360  
|||||  
QY 361 HRDKTWGDVVEEFPERPERFENPSAIPQHAFKPFNGQORACIGQOFALHEATLVLGMLKH 420  
|||||  
Db 361 HRDKTWGDVVEEFPERPERFENPSAIPQHAFKPFNGQORACIGQOFALHEATLVLGMLKH 420  
|||||  
QY 421 FDFEDHTNYELDIKETLTLLKPEGVYVKAQSKKIPLGGI 458  
|||||  
Db 421 FDFEDHTNYELDIKETLTLLKPEGVYVKAQSKKIPLGGI 458  
|||||

## RESULT 15

US-09-791-537-8264  
; Sequence 8264, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8264  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: pdb 2B1HA  
US-09-791-537-8264

Query Match 43.4%; Score 455; DB 21; Length 455;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPQKTFGELKKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60  
|||||  
Db 1 TIKEMPQKTFGELKKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60  
|||||  
QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 120  
|||||  
Db 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV 120  
|||||  
QY 121 DIAVOLVQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNRYNSFYRDQPHFITSWVRA 180  
|||||  
Db 121 DIAVOLVQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNRYNSFYRDQPHFITSWVRA 180  
|||||  
QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG 240  
|||||  
Db 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG 240  
|||||  
QY 241 KPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVQLQAAEAAARVLD 300  
|||||  
Db 241 KPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVQLQAAEAAARVLD 300  
|||||  
QY 301 PVPYSYQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELMLVLPOL 360  
|||||  
Db 301 PVPYSYQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELMLVLPOL 360  
|||||  
QY 361 HRDKTWGDVVEEFPERPERFENPSAIPQHAFKPFNGQORACIGQOFALHEATLVLGMLKH 420  
|||||  
Db 361 HRDKTWGDVVEEFPERPERFENPSAIPQHAFKPFNGQORACIGQOFALHEATLVLGMLKH 420  
|||||  
QY 421 FDFEDHTNYELDIKETLTLLKPEGVYVKAQSKKIPL 455  
|||||  
Db 421 FDFEDHTNYELDIKETLTLLKPEGVYVKAQSKKIPL 455  
|||||

Search completed: May 29, 2003, 08:37:24  
Job time : 301 secs



Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	17	1.6	1073	6	US-10-156-761-8117	Sequence 8117, Ap	
2	16	1.5	659	6	US-10-369-493-2518	Sequence 2518, Ap	
3	16	1.5	678	6	US-10-369-493-2517	Sequence 2517, Ap	
4	15	1.4	592	6	US-10-369-493-4874	Sequence 4874, Ap	
5	15	1.4	592	6	US-10-369-493-7634	Sequence 7634, Ap	
6	15	1.4	1077	6	US-10-214-446-24	Sequence 24, Appl	
7	12	1.1	504	6	US-10-156-761-14954	Sequence 14954, A	
8	12	1.1	676	6	US-10-219-051B-12757	Sequence 12757, A	
9	12	1.1	677	7	US-60-440-068-572	Sequence 572, App	
10	12	1.1	682	6	US-10-148-907A-23	Sequence 23, Appl	
11	12	1.1	691	6	US-10-369-493-22034	Sequence 22034, A	
12	11	1.0	689	6	US-10-424-599-187294	Sequence 187294, A	
13	11	1.0	691	6	US-10-424-599-191313	Sequence 191313, A	
14	11	1.0	1352	6	US-10-156-761-9867	Sequence 9867, Ap	
15	10	1.0	588	6	US-10-188-533B-14	Sequence 14, Appl	
16	10	1.0	588	6	US-10-188-533C-14	Sequence 14, Appl	
17	10	1.0	629	6	US-10-092-411A-4394	Sequence 4394, Ap	
18	10	1.0	719	6	US-10-425-114-70174	Sequence 70174, A	
19	10	1.0	1199	7	US-60-452-680-23982	Sequence 23982, A	
20	10	1.0	1199	7	US-60-453-135-14960	Sequence 14960, A	
21	10	1.0	1199	7	US-60-453-050-14960	Sequence 14960, A	
22	10	1.0	1199	7	US-60-455-444-8116	Sequence 8116, Ap	
23	10	1.0	1199	7	US-60-465-241-8116	Sequence 8116, Ap	
24	10	1.0	1429	5	US-09-661-258-2	Sequence 2, Appl	
25	10	1.0	1434	5	US-09-661-258-1	Sequence 1, Appl	
26	9	0.9	199	5	US-09-675-784A-13060	Sequence 13060, A	

; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 2518  
; LENGTH: 659  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-10-369-493-2518

Query Match 1.5%; Score 16; DB 6; Length 659;  
Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGGTGVAPRGGFV 914  
|||||  
Db 515 INVPGGTGVAPRGGFV 530

RESULT 3  
US-10-369-493-2517  
; Sequence 2517, Application US/10369493  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 2517  
; LENGTH: 678  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-10-369-493-2517

Query Match 1.5%; Score 16; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 6.4e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGGTGVAPRGGFV 914  
|||||  
Db 534 INVPGGTGVAPRGGFV 549

RESULT 4  
US-10-369-493-4874  
; Sequence 4874, Application US/10369493  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 4874  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Burkholderia fungorum  
US-10-369-493-4874

Query Match 1.4%; Score 15; DB 6; Length 592;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGGTGVAPRGGFV 913  
|||||  
Db 449 INVPGGTGVAPRGGFV 463

RESULT 5  
US-10-369-493-7634  
; Sequence 7634, Application US/10369493  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 7634  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Burkholderia cepacia  
US-10-369-493-7634

Query Match 1.4%; Score 15; DB 6; Length 592;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGGTGVAPRGGFV 913  
|||||  
Db 449 INVPGGTGVAPRGGFV 463

RESULT 6  
US-10-214-446-24  
; Sequence 24, Application US/10214446  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, David  
; APPLICANT: Burk, Mark J.  
; APPLICANT: Hitchman, Tim  
; APPLICANT: Pujol, Catherine  
; APPLICANT: Richardson, Toby  
; APPLICANT: Short, Jay M.  
; TITLE OF INVENTION: P450 ENZYMES, NUCLEIC ACIDS ENCODING  
; FILE REFERENCE: 09010-500001  
; CURRENT APPLICATION NUMBER: US/10/214,446  
; CURRENT FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: US 60/309,497  
; PRIOR FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 1077  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Obtained from an environmental sample  
US-10-214-446-24

Query Match 1.4%; Score 15; DB 6; Length 1077;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 TFLIAGHETTSGLLS 274

Db 266 TFLIAGHETTSGLIS 280  
|||||

RESULT 7  
US-10-156-761-14954  
; Sequence 14954, Application US/10156761  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 14954  
; LENGTH: 504  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-14954

Query Match 1.1% Score 12; DB 6; Length 504;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 404 QFALHEATVIG 415  
Db 430 QFALHEATVIG 441  
|||||

RESULT 8  
US-10-219-051B-12757  
; Sequence 12757, Application US/10219051B  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; APPLICANT: Hospital / Bayer AG  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: Lea 35693 Foreign Countries  
; CURRENT APPLICATION NUMBER: US/10/219,051B  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/312,147  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US 60/346,382  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/333,347  
; PRIOR FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 14715  
; SOFTWARE: Perl script  
; SEQ ID NO 12757  
; LENGTH: 676  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: SWISS-Prot / BAB18572  
; DATABASE ENTRY DATE: 2002-06-15  
US-10-219-051B-12757

Query Match 1.1% Score 12; DB 6; Length 676;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPF 910  
Db 528 IMVPGTGVAPF 539  
|||||

RESULT 9  
US-60-440-068-572  
; Sequence 572, Application US/60440068  
; GENERAL INFORMATION:  
; APPLICANT: NADLER, STEVEN G.  
; APPLICANT: CARMAN, JULIE  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE  
; TITLE OF INVENTION: NF-KB PATHWAY  
; FILE REFERENCE: 3053-4191  
; CURRENT APPLICATION NUMBER: US/60/440,068  
; CURRENT FILING DATE: 2003-01-14  
; NUMBER OF SEQ ID NOS: 746  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 572  
; LENGTH: 677  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-440-068-572

Query Match 1.1% Score 12; DB 7; Length 677;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPF 910  
Db 529 IMVPGTGVAPF 540  
|||||

RESULT 10  
US-10-148-907A-23  
; Sequence 23, Application US/10148907A  
; GENERAL INFORMATION:  
; APPLICANT: Novartis AG  
; TITLE OF INVENTION: Compositions and Methods for Halogenation Reactions  
; FILE REFERENCE: S-31082A  
; CURRENT APPLICATION NUMBER: US/10/148,907A  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 60/228801  
; PRIOR FILING DATE: 1999-12-15  
; PRIOR APPLICATION NUMBER: US 60/219343  
; PRIOR FILING DATE: 2000-01-03  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 682  
; TYPE: PRT  
; ORGANISM: Oryctolagus cuniculus  
US-10-148-907A-23

Query Match 1.1% Score 12; DB 6; Length 682;  
Best Local Similarity 100.0%; Pred. No. 0.0085;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 IMVPGTGVAPF 910  
Db 533 IMVPGTGVAPF 544  
|||||

RESULT 11  
US-10-369-493-22034  
; Sequence 22034, Application US/10369493  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 22034  
; LENGTH: 691  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-369-493-22034

Query Match 1.1%; Score 12; DB 6; Length 691;  
Best Local Similarity 100.0%; Pred. No. 0.0086;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 902 GPGTGVAPRGF 913  
DB 540 GPGTGVAPRGF 551  
|||||

RESULT 12  
US-10-424-599-187294  
; Sequence 187294, Application US/10424599  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 187294  
; LENGTH: 689  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(689)  
; OTHER INFORMATION: unsure at all xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_140138C.1.pap  
US-10-424-599-187294

Query Match 1.0%; Score 11; DB 6; Length 689;  
Best Local Similarity 100.0%; Pred. No. 0.091;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSPR 836  
DB 466 PRYSSSPR 476  
|||||

RESULT 13  
US-10-424-599-191313  
; Sequence 191313, Application US/10424599  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 191313  
; LENGTH: 691  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_14776C.1.pap  
US-10-424-599-191313

Query Match 1.0%; Score 11; DB 6; Length 691;  
Best Local Similarity 100.0%; Pred. No. 0.092;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSPR 836  
DB 468 PRYSSSPR 478  
|||||

RESULT 14  
US-10-156-761-9867  
; Sequence 9867, Application US/10156761  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: HORIKAWA, JUN  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 9867  
; LENGTH: 1352  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-9867

Query Match 1.0%; Score 11; DB 6; Length 1352;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 900 MVPGTGVAPF 910  
DB 1210 MVPGTGVAPF 1220  
|||||

RESULT 15  
US-10-188-523B-14  
; Sequence 14, Application US/10188523B  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Xiao-Song  
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID  
; FILE REFERENCE: BC1009 US DIVCIP  
; CURRENT APPLICATION NUMBER: US/10/188,523B  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: US 09/627,216  
; PRIOR FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: US 60/147,719  
; PRIOR FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 14  
; LENGTH: 588  
; TYPE: PRT  
; ORGANISM: Helianthus tuberosus  
US-10-188-523B-14

Query Match 1.0%; Score 10; DB 6; Length 588;  
Best Local Similarity 100.0%; Pred. No. 0.84;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 PRYSSSPR 835

Db           |||||  
          365 PRYSSSP 374

Search completed: May 29, 2003, 08:39:13  
Job time : 106 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:37:32 ; Search time 99 Seconds  
(without alignments)  
2181.186 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 1048

Sequence: 1 TIKEMPQKTFGELKNLPL.....RLWLQLEKGRYKDVWAG 1048

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_prodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	2.7	29	Q9AE23	Q9ae23 bacillus me
2	17	1.6	730	Q8X1W0	Q8x1w0 coriolus ve
3	15	1.4	693	Q00141	Q00141 aspergillus
4	14	1.3	690	Q9HG14	Q9hg14 phanerocha
5	14	1.3	736	Q9HDP2	Q9hdg2 phanerocha
6	13	1.2	558	Q94613	Q94613 schizosacch
7	13	1.2	597	Q9UHB4	Q9uhb4 homo sapien
8	13	1.2	597	Q96BC6	Q96bc6 homo sapien
9	13	1.2	605	Q32214	Q32214 bacillus su
10	13	1.2	607	Q9KF76	Q9kf76 bacillus ha
11	13	1.2	629	Q9P4E1	Q9p4e1 cunningham
12	13	1.2	671	Q9HVV3	Q9hvv3 rhizopus st
13	13	1.2	710	Q9P4E2	Q9p4e2 cunningham
14	13	1.2	1066	Q9Y8G7	Q9y8g7 fusarium ox
15	12	1.1	527	Q9RD76	Q9rd76 streptomyce
16	12	1.1	696	Q8ROY3	Q8roy3 mus musculus

17	12	1.1	759	3	Q9C498	Q9c498 rhodotorula
18	11	1.0	506	10	Q96560	Q96560 helianthus
19	11	1.0	681	10	Q48937	Q48937 petroselinu
20	11	1.0	692	10	Q43235	Q43235 vicia sativ
21	11	1.0	692	10	Q9AU08	Q9au08 populus bal
22	11	1.0	692	10	Q9SB48	Q9sb48 arabidopsis
23	11	1.0	699	10	Q48938	Q48938 petroselinu
24	11	1.0	703	10	Q8VX49	Q8vx49 triticum ae
25	11	1.0	704	10	Q04434	Q04434 pisum sativ
26	11	1.0	712	10	Q9AU06	Q9au06 populus bal
27	11	1.0	719	10	Q40916	Q40916 pseudotsuga
28	11	1.0	1115	3	Q9HGE0	Q9hg0 gibberella
29	10	1.0	238	10	Q42830	Q42830 helianthus
30	10	1.0	541	5	Q961A7	Q961a7 drosophila
31	10	1.0	582	5	Q9VJS5	Q9vjs5 drosophila
32	10	1.0	585	5	Q902Y8	Q9uzy8 caenorhabdi
33	10	1.0	588	10	Q96561	Q96561 helianthus
34	10	1.0	612	16	Q9PD80	Q9pd80 xyella fas
35	10	1.0	614	16	Q9KUX4	Q9kux4 vibrio chol
36	10	1.0	683	10	Q24424	Q24424 papaver som
37	10	1.0	687	5	Q9NKV3	Q9nkvs bombyx mori
38	10	1.0	712	10	Q9AU07	Q9au07 populus bal
39	9	0.9	120	2	Q85652	Q85652 micromonosp
40	9	0.9	120	2	Q85654	Q85654 pseudonocar
41	9	0.9	317	10	Q9SB29	Q9sb29 oryza sativ
42	9	0.9	327	10	Q41736	Q41736 zea mays (m
43	9	0.9	506	10	Q9ATU8	Q9atu8 lolium rigi
44	9	0.9	513	10	Q9ATU7	Q9atu7 lolium rigi
45	9	0.9	701	5	P91655	P91655 drosophila

#### ALIGNMENTS

##### RESULT 1

Q9AE23 PRELIMINARY; PRT; 29 AA.  
ID Q9AE23  
AC Q9AE23;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Cytochrome P450BM-3 (Fragment).  
OS Bacillus megaterium.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92184811; PubMed=1544926;  
RA Shaw G.C., Fulco A.J.;  
RT "Barbiturate-mediated regulation of expression of the cytochrome  
RT P450BM-3 gene of Bacillus megaterium by Bm3R1 protein.";  
RL J. Biol. Chem. 267:5515-5526(1992).  
DR EMBL; S87512; AAK19020.1; -;  
FT NON\_TER 29  
SQ SEQUENCE 29 AA; 3283 MW; D97C2CFB57450EE8 CRC64;

Query Match 2.7%; Score 28; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 8.1e-21;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPQKTFGELKNLPLLTNDKPVQA 28  
Db 2 TIKEMPQKTFGELKNLPLLTNDKPVQA 29

##### RESULT 2

Q8X1W0 PRELIMINARY; PRT; 730 AA.  
ID Q8X1W0  
AC Q8X1W0;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Cytochrome P450 oxidoreductase.  
CPR.  
ON Coriolus versicolor.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Aphyllophorales; Coriolus.  
OX NCBI\_TaxID=57466;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ichinose H., Wariishi H., Tanaka H.;  
RT "Identification of cytochrome P450 oxidoreductase from white-rot  
basidiomycete Coriolus versicolor.";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB063368; BAB83588.1; -  
DR InterPro: IPR003097; FAD\_binding.  
DR InterPro: IPR001094; Flavodoxin.  
DR InterPro: IPR001226; Flavodoxin.  
DR InterPro: IPR001433; Oxid\_FAD/NAD(P).  
DR Pfam: PF00667; FAD\_binding; 1.  
DR Pfam: PF00258; flavodoxin; 1.  
DR Pfam: PF00175; NAD\_binding; 1.  
DR PRINTS: PR00369; FLAVODOXIN.  
DR PRINTS: PR00371; FPNCR.  
SQ SEQUENCE 730 AA; 80742 MW; DB6FBC5FF3B15730 CRC64;  
Query Match 1.6%; Score 17; DB 3; Length 730;  
Best Local Similarity 100.0%; Pred. No. 4.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 899 INVGGTGVAPRGRFVQ 915  
DB 566 INVGGTGVAPRGRFVQ 582  
RESULT 3  
Q00141 ID Q00141 PRELIMINARY; PRT; 693 AA.  
AC Q00141;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE NADPH cytochrome P450 oxidoreductase.  
OS Aspergillus niger.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
OX NCBI\_TaxID=5061;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA van den Brink J., van Zeijl C., van den Hondel C., van Gorcom R.;  
RT "Cloning and characterization of the NADPH cytochrome P450  
oxidoreductase (cprA) gene of Aspergillus niger."  
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Z26938; CA81550.1; -  
DR HSP: PL6435; IBIC.  
DR InterPro: IPR003097; FAD\_binding.  
DR InterPro: IPR001094; Flavodoxin.  
DR InterPro: IPR001226; Flavodoxin.  
DR InterPro: IPR001709; FPN\_cyt\_redctse.  
DR InterPro: IPR001433; Oxid\_FAD/NAD(P).  
DR Pfam: PF00667; FAD\_binding; 1.  
DR Pfam: PF00258; flavodoxin; 1.  
DR Pfam: PF00175; NAD\_binding; 1.  
DR PRINTS: PR00369; FLAVODOXIN.  
DR PRINTS: PR00371; FPNCR.  
KW NADP.  
SQ SEQUENCE 693 AA; 77072 MW; 1BEF35D4FC767674 CRC64;  
Query Match 1.4%; Score 15; DB 3; Length 693;  
Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVGGTGVAPRGRF 913  
DB 544 INVGGTGVAPRGRF 558  
RESULT 4  
Q9HG14 ID Q9HG14 PRELIMINARY; PRT; 690 AA.  
AC Q9HG14;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4)  
(Fragment).  
OS Phanerochaete chrysosporium.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Aphyllophorales; Corticiaceae; Phanerochaete.  
OX NCBI\_TaxID=5306;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yadav J.S., Loper J.C.;  
RT "Cytochrome P450 oxidoreductase gene and its differentially terminated  
cDNAs from the white rot fungus Phanerochaete chrysosporium.";  
RL Curr. Genet. 37:65-73(2000).  
DR EMBL: AF193062; AAG31351.1; -  
DR HSP: P00388; IAWO.  
DR InterPro: IPR003097; FAD\_binding.  
DR InterPro: IPR001094; Flavodoxin.  
DR InterPro: IPR001226; Flavodoxin.  
DR InterPro: IPR001709; FPN\_cyt\_redctse.  
DR InterPro: IPR001433; Oxid\_FAD/NAD(P).  
DR Pfam: PF00667; FAD\_binding; 1.  
DR Pfam: PF00258; flavodoxin; 1.  
DR Pfam: PF00175; NAD\_binding; 1.  
DR PRINTS: PR00369; FLAVODOXIN.  
DR PRINTS: PR00371; FPNCR.  
KW Oxidoreductase.  
FT NON\_TER 1  
SQ SEQUENCE 690 AA; 76880 MW; 48B7D25BEC0F06B5 CRC64;  
Query Match 1.3%; Score 14; DB 3; Length 690;  
Best Local Similarity 100.0%; Pred. No. 5.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 902 GPGTGVAPRGRFVQ 915  
DB 528 GPGTGVAPRGRFVQ 541  
RESULT 5  
Q9HDG2 ID Q9HDG2 PRELIMINARY; PRT; 736 AA.  
AC Q9HDG2;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4).  
OS Phanerochaete chrysosporium.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Aphyllophorales; Corticiaceae; Phanerochaete.  
OX NCBI\_TaxID=5306;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yadav J.S., Loper J.C.;  
RT "Cytochrome P450 oxidoreductase gene and its differentially terminated  
cDNAs from the white rot fungus Phanerochaete chrysosporium.";  
RL Curr. Genet. 37:65-73(2000).



DR EMBL; AF193061; AAC31350.1; -;  
 DR EMBL; AF193060; AAC31349.1; -;  
 DR HSSP; P00388; IAMO.  
 DR InterPro; IPR003097; FAD\_binding.  
 DR InterPro; IPR001094; Flavodoxin\_like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001709; FPN\_cyt\_redtse.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
 DR Pfam; PF00175; NAD\_binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 KW Oxidoreductase.  
 SQ SEQUENCE 736 AA; 81627 MW; AC45F12C96198AB1 CRC64;

Query Match 1.3%; Score 14; DB 3; Length 736;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 902 GPGTGVAPFRGFVQ 915  
 Db 574 GPGTGVAPFRGFVQ 587  
 [|||||]

RESULT 6  
 O94613 PRELIMINARY; PRT; 558 AA.  
 AC O94613;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Putative NADPH-cytochrome P450 reductase (EC 1.6.2.4).  
 GN SPAC1296.06.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-972;  
 RA Wood V., Barrell B.G., Rajandream M.A., Harris D., Seeger K.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
 CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5 (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME - NADP(+) + 2  
 CC FERROCYTOCHROME.  
 CC -1- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FMN (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE ER  
 CC MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION (BY SIMILARITY).  
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
 CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
 CC REDUCTASE.

DR EMBL; AL035439; CAB36512.2; -;  
 DR HSSP; P00388; IAMO.  
 DR InterPro; IPR003097; FAD\_binding.  
 DR InterPro; IPR001094; Flavodoxin\_like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001709; FPN\_cyt\_redtse.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
 DR Pfam; PF00175; NAD\_binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 DR Hypothetical protein; Oxidoreductase; Flavoprotein; FMN; FAD; NADP;  
 KW Endoplasmic reticulum; Membrane.  
 FT NP\_BIND 524 542 NADP (RIBOSE PART) (BY SIMILARITY).  
 SQ SEQUENCE 558 AA; 64199 MW; 12D64991612E7E00 CRC64;

Query Match 1.2%; Score 13; DB 3; Length 558;  
 Best Local Similarity 100.0%; Pred. No. 0.00046;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 897 PLIMVPGTGVAP 909  
 Db 414 PLIMVPGTGVAP 426  
 [|||||]

RESULT 7  
 O9UHB4 PRELIMINARY; PRT; 597 AA.  
 AC O9UHB4;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE NADPH-dependent FMN and FAD containing oxidoreductase.  
 GN NRI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20092928; PubMed=10625700;  
 RA Paine M.J., Garner A.P., Powell D., Sibbald J., Sales M., Pratt N.,  
 RA Smith T., Tew D.G., Wolf C.R.;  
 RT "Cloning and Characterization of a Novel Human Dual Flavin  
 RT Reductase";  
 RL J. Biol. Chem. 275:1471-1478(2000).  
 DR EMBL; AF199509; AAF25205.1; -;  
 DR HSSP; P00388; IAMO.  
 DR InterPro; IPR003097; FAD\_binding.  
 DR InterPro; IPR001094; Flavodoxin\_like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001709; FPN\_cyt\_redtse.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
 DR Pfam; PF00175; NAD\_binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 SQ SEQUENCE 597 AA; 66762 MW; 0D1340D7280A4D8F CRC64;

Query Match 1.2%; Score 13; DB 4; Length 597;  
 Best Local Similarity 100.0%; Pred. No. 0.00049;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 899 IMVPGTGVAPFR 911  
 Db 454 IMVPGTGVAPFR 466  
 [|||||]

RESULT 8  
 O96BC6 PRELIMINARY; PRT; 597 AA.  
 AC O96BC6;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE NADPH-dependent FMN and FAD containing oxidoreductase.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SKIN;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC015735; AAH15735.1; -;  
 DR InterPro; IPR003097; FAD\_binding.  
 DR InterPro; IPR001226; Flavodoxin.

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DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00667; FAD_binding; 1.
DR Pfam: PF00258; Flavodoxin; 1.
DR Pfam: PF00175; NAD_binding; 1.
SQ SEQUENCE 597 AA; 66776 MW; E1C340CF93A95534 CRC64;

Query Match 1.2%; Score 13; DB 4; Length 597;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGTGVAPR 911
Db 454 INVPGTGVAPR 466

RESULT 9
O32214 PRELIMINARY; PRT; 605 AA.
AC O32214;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Sulfite reductase [NADPH] flavoprotein alpha-component-like protein
DE (YVGR protein).
GN YVGR.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriest B., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denisot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T., Yata K.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99121; CAB15349.1; -.
DR HSSP; P00388; 1AMO.
DR InterPro: IPR003097; FAD_binding.
DR InterPro: IPR001094; Flavodoxin_like.

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DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00667; FAD_binding; 1.
DR Pfam: PF00258; Flavodoxin; 1.
DR Pfam: PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
KW Complete proteome.
SQ SEQUENCE 605 AA; 67259 MW; 486F512C0AED6217 CRC64;

Query Match 1.2%; Score 13; DB 16; Length 605;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGTGVAPR 911
Db 462 INVPGTGVAPR 474

RESULT 10
O9KF76 PRELIMINARY; PRT; 607 AA.
AC O9KF76;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Sulfite reductase (NADPH).
GN BH0609.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirano C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001509; BAB04328.1; -.
DR HSSP; P00388; 1AMO.
DR InterPro: IPR003097; FAD_binding.
DR InterPro: IPR001094; Flavodoxin_like.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001709; FPN_cyt_redctase.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00258; Flavodoxin; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Complete proteome.
SQ SEQUENCE 607 AA; 67865 MW; 3CD1B0FAA1DBFFBE CRC64;

Query Match 1.2%; Score 13; DB 16; Length 607;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 INVPGTGVAPR 911
Db 464 INVPGTGVAPR 476

RESULT 11
O9P4E1 PRELIMINARY; PRT; 629 AA.
AC O9P4E1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4)

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(Fragment).  
 DE Cunninghamella echinulata.  
 OS Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;  
 OC Cunninghamellaceae; Cunninghamella.  
 OX NCBI\_TaxID=76405;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 26878;  
 RX MEDLINE=20145435; PubMed=10679206;  
 RA Yadav J.S., Loper J.C.;  
 RT "Cloning and characterization of the cytochrome P450 oxidoreductase  
 gene from the zygomycete fungus Cunninghamella.";  
 RL Biochem. Biophys. Res. Commun. 268:345-353(2000).  
 DR EMBL; AF195660; AAF89959.1; -;  
 DR HSSP; P16435; 1B1C.  
 DR InterPro; IPR003097; FAD\_binding.  
 DR InterPro; IPR001094; Flavodoxin\_like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001709; FPN\_cyt\_redctse.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 DR Oxidoreductase.  
 KW Oxidoreductase.  
 FT NON\_TER 1  
 SQ SEQUENCE 629 AA; 71388 MW; EC63589C857965A5 CRC64;  
 Query Match 1.2%; Score 13; DB 3; Length 629;  
 Best Local Similarity 100.0%; Pred. No. 0.00052;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 902 GPGTGVAAPFRGFV 914  
 Db 482 GPGTGVAAPFRGFV 494  
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 RESULT 12  
 Q9HFV3 PRELIMINARY; PRT; 671 AA.  
 AC Q9HFV3; 2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE NADPH cytochrome P450 oxidoreductase isoenzyme 1 (EC 1.6.2.4).  
 OS Rhizopus stolonifer (Rhizopus nigricans).  
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;  
 OC Rhizopus.  
 OX NCBI\_TaxID=4846;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunik B., Truan G., Breskvar K., Pompon D.;  
 RT "Function cloning based on azole resistance in S. cerevisiae and  
 characterization of R. nigricans redox carriers differentially  
 involved in P450 dependent response to progesterone stress.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF290425; AAG23833.1; -;  
 DR HSSP; P00388; IAWO  
 DR InterPro; IPR003097; FAD\_binding.  
 DR InterPro; IPR001094; Flavodoxin\_like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001709; FPN\_cyt\_redctse.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
 DR PRINTS; PR00175; NAD\_binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 DR Oxidoreductase.  
 KW Oxidoreductase.  
 SQ SEQUENCE 671 AA; 76205 MW; AAC1B236ACA5F88B CRC64;  
 Query Match 1.2%; Score 13; DB 3; Length 671;

Best Local Similarity 100.0%; Pred. No. 0.00055;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 902 GPGTGVAAPFRGFV 914  
 Db 527 GPGTGVAAPFRGFV 539  
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 RESULT 13  
 Q9P4E2 PRELIMINARY; PRT; 710 AA.  
 AC Q9P4E2; 2001 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4).  
 OS Cunninghamella elegans.  
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;  
 OC Cunninghamellaceae; Cunninghamella.  
 OX NCBI\_TaxID=4853;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 36112;  
 RX MEDLINE=20145435; PubMed=10679206;  
 RA Yadav J.S., Loper J.C.;  
 RT "Cloning and characterization of the cytochrome P450 oxidoreductase  
 gene from the zygomycete fungus Cunninghamella.";  
 RL Biochem. Biophys. Res. Commun. 268:345-353(2000).  
 DR EMBL; AF195659; AAF89958.1; -;  
 DR HSSP; P16435; 1B1C.  
 DR InterPro; IPR003097; FAD\_binding.  
 DR InterPro; IPR001094; Flavodoxin\_like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001709; FPN\_cyt\_redctse.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 DR Oxidoreductase.  
 KW Oxidoreductase.  
 SQ SEQUENCE 710 AA; 80021 MW; 8B3443AF5CDA3565 CRC64;  
 Query Match 1.2%; Score 13; DB 3; Length 710;  
 Best Local Similarity 100.0%; Pred. No. 0.00058;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 902 GPGTGVAAPFRGFV 914  
 Db 564 GPGTGVAAPFRGFV 576  
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 RESULT 14  
 Q9Y8G7 PRELIMINARY; PRT; 1066 AA.  
 AC Q9Y8G7; 2001 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Bifunctional P-450:NADPH-P450 reductase protein (Fatty acid omega-  
 DE hydroxylase) (P450foxy) [Includes: cytochrome P450 505 (EC 1.14.14.1);  
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4)].  
 GN CYP505.  
 OS Fusarium oxysporum.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreales; Mitosporic Hypocreales; Fusarium.  
 OX NCBI\_TaxID=5507;  
 RN [1]  
 RP SEQUENCE FROM N.A.; PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.  
 RC STRAIN=MT-811;  
 RX MEDLINE=20564350; PubMed=10995755;  
 RA Kitazume T., Takaya N., Nakayama N., Shoun H.;  
 RT "Fusarium oxysporum fatty-acid subterminal hydroxylase (CYP505) is a

membrane-bound eukaryotic counterpart of Bacillus megaterium  
 Cytochrome P450BM3.<sup>2</sup>  
 J. Biol. Chem. 275:39734-39740(2000).  
 [2]  
 FUNCTION, AND SUBCELLULAR LOCATION.  
 STRAIN-MT-811;  
 MEDLINE-96271003; PubMed-8830036;  
 Nakayama N., Takemae A., Shoun H.;  
 "Cytochrome P450foxy, a catalytically self-sufficient fatty acid  
 hydroxylase of the fungus Fusarium oxysporum."  
 J. Biochem. 119:435-440(1996).  
 CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. SHOWS HIGHEST  
 ACTIVITY TOWARD FATTY ACIDS WITH A CHAIN LENGTH OF 12-14 CARBONS.  
 THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
 TO CYTOCHROME P450.  
 CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) -> ROH +  
 OXIDIZED FLAVOPROTEIN + H(2)O.  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) + 2  
 FERROCYTOCHROME.  
 CC -1- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FMN (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME  
 P450 FAMILY.  
 DR EMBL; AB030037; BAA82526.1; -.  
 DR HSSP; P14779; IBVY.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR InterPro; IPR003097; FAD\_binding.  
 DR InterPro; IPR001094; Flavodoxin\_like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001709; FPN\_cyt\_redctase.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
 DR Pfam; PF00175; NAD\_binding; 1.  
 DR Pfam; PF00067; p450; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KW Heme; Monooxygenase; Oxidoreductase; Membrane; Electron transport;  
 KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP.  
 FT DOMAIN 1 480 CYTOCHROME P450  
 FT BINDING 481 1066 NADPH-P-450 REDUCTASE.  
 FT BINDING 407 407 HEME (BY SIMILARITY).  
 SQ SEQUENCE 1066 AA; 117925 MW; 6B8123698C23DBA CRC64;  
 Query Match 1.2%; Score 13; DB 3; Length 1066;  
 Best Local Similarity 100.0%; Pred. No. 0.00085;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 259 ITFLIAGHETTS 271  
 Db 261 ITFLIAGHETTS 273  
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 Q9RD76 PRELIMINARY; PRT; 527 AA.  
 AC Q9RD76;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Putative cytochrome P450.  
 GN SC00801 OR SCE43.12.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_Taxid=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA Saunders D.C., Harris D.;  
 Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;  
 Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RX MEDLINE-97000351; PubMed-8843436;  
 RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,  
 Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmid and a detailed genetic and physical map for  
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."  
 RL Mol. Microbiol. 21:77-96(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2) / M145;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
 Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,  
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 coelicolor A3(2)."  
 RL Nature 417:141-147(2002).  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL; AL136502; CAB66201.1; -.  
 DR HSSP; P14779; IBVY.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR InterPro; IPR000217; Tubulin.  
 DR Pfam; PF00067; p450; 1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; UNKNOWN\_1.  
 DR PROSITE; PS00227; TUBULIN; 1.  
 KW Heme; Monooxygenase; Oxidoreductase.  
 SQ SEQUENCE 527 AA; 57741 MW; 4A612C1B7A894780 CRC64;  
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 Db 444 QFALHEATLVLG 455  
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 Job time : 100 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:22:16; Search time 74 Seconds  
(without alignments)  
1887.117 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 5457

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Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	5457	100.0	1048	22 AAB46855	B. megaterium cyto
3	5457	100.0	1048	22 AAB46856	B. megaterium cyto
4	5457	100.0	1049	21 AAY93566	Amino acid sequenc
5	5457	100.0	1049	22 AAB31882	Amino acid sequenc
6	5450	99.9	1048	22 AAB31979	Amino acid sequenc
7	5449	99.9	1049	22 AAB72208	Bacillus megateriu
8	5444	99.8	1048	22 AAB31980	Amino acid sequenc
9	5440	99.7	1048	22 AAB31981	Amino acid sequenc
10	3154.5	57.8	1085	12 AAR11604	P450 17-alpha/P450

11	971.5	17.8	1144	9 AAP81334	Expression prod. o
12	968.5	17.7	1150	9 AAP81337	Expression prod. o
13	962.5	17.6	1150	9 AAP81335	Expression prod. o
14	916.5	16.8	1162	9 AAP81336	Expression prod. o
15	906.5	16.6	1132	9 AAP81338	Expression prod. o
16	778.5	14.3	678	23 ABB57261	Mouse ischaemic co
17	774.5	14.2	678	8 AAP70380	Plasmid pRF1 rat 1
18	772.5	14.2	678	8 AAP70378	NADPH cytochrome P
19	769	14.1	679	8 AAP70546	Sequence of rabbit
20	769	14.1	682	22 AAB82516	Rabbit NADH cytoch
21	766	14.0	680	22 AAU27786	Human full-length
22	766	14.0	685	22 AAU27958	Human contig polyp
23	761	13.9	677	22 AAB73901	Human derived cyto
24	761	13.9	677	22 AAB73902	Human derived cyto
25	747	13.7	676	20 AAY42286	Human P450 reducta
26	747	13.7	676	20 AAY27398	Human P450 reducta
27	747	13.7	676	23 AAO17538	Human P450(cytochr
28	746	13.7	671	14 AAR43583	Plant NADPH cytoch
29	737.5	13.5	616	20 AAY42287	Human anchorless P
30	737.5	13.5	616	20 AAY27399	Human P450 reducta
31	726	13.3	623	9 AAP81339	Expression prod. o
32	725.5	13.3	679	22 ABB64462	Drosophila melanog
33	723.5	13.3	1169	16 AAR76544	Mitochondrial cyto
34	711.5	13.0	683	20 AAW85682	Poppy cytochrome P
35	711.5	13.0	883	20 AAW85680	Poppy cytochrome P
36	710.5	13.0	692	14 AAR43581	Plant NADPH cytoch
37	709	13.0	697	21 AAG35842	Arabidopsis thalia
38	709	13.0	701	21 AAG35841	Arabidopsis thalia
39	709	13.0	711	21 AAG35840	Arabidopsis thalia
40	705.5	12.9	588	23 AAE20656	Helianthus tuberos
41	705.5	12.9	588	23 AAE16392	Helianthus tuberos
42	703.5	12.9	704	20 AAW85683	Poppy cytochrome P
43	703.5	12.9	852	20 AAW85681	Poppy cytochrome P
44	695.5	12.7	712	14 AAR43582	Plant NADPH cytoch
45	678	12.4	1429	14 AAR44489	Sequence of all or

## ALIGNMENTS

### RESULT 1

AAB31978  
ID AAB31978 standard; Protein; 1048 AA.

XX AC AAB31978;

XX AC AAB31978;

DT 15-MAY-2001 (first entry)

XX DE Amino acid sequence of a Bacillus P450 monooxygenase protein.

XX KW Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.

XX OS Bacillus megaterium.

XX PN WO200107630-A1.

XX PD 01-FEB-2001.

XX PF 27-JUL-2000; 2000WO-EP07253.

XX PR 27-JUL-1999; 99DE-1035115.

XX PR 18-NOV-1999; 99DE-1055605.

XX PR 22-MAR-2000; 2000DE-1014085.

XX PA (BADI ) BASF AG.

XX PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;

XX PI Li Q;

XX XX WPI; 2001-182800/18.

XX DR N-PSDB; AAF54832.

XX PT Cytochrome P450 monooxygenase for oxidizing organic compounds, useful

PT especially for converting indole to indigo, has wide substrate range -  
 XX Claim 3; Page 35-39; 54pp; German.  
 CC The present sequence represents a cytochrome P450 monooxygenase. The  
 CC specification describes a modified cytochrome P450 monooxygenase which  
 CC can oxidize at least one of the following types of substrates:  
 CC optionally substituted mono- or poly-cyclic aromatic heterocyclics  
 CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or  
 CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or  
 CC optionally substituted cycloalkanes or cycloalkenes. The modified  
 CC cytochrome P450 monooxygenase are specifically used to oxidize indole  
 CC to indigo and indorubicin. However, they may be used to oxidize many  
 CC other substrates.  
 XX  
 SQ Sequence 1048 AA;

Query Match 100.0%; Score 5457; DB 22; Length 1048;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMQPKTFGKLNPLNTDKPVQALMKIADLGEIFKFEAPGRVTRYLSSQRLIKE 60  
 DB 1 TIKEMQPKTFGKLNPLNTDKPVQALMKIADLGEIFKFEAPGRVTRYLSSQRLIKE 60  
 QY 61 ACDESFRDKNLSQALFVRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAMKGYHAMV 120  
 DB 61 ACDESFRDKNLSQALFVRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAMKGYHAMV 120  
 QY 121 DIAVLQVQWERLNADLHEIPEVDMTRRLDITGLCGFNRYRNSFYRDQPHPTSMVRA 180  
 DB 121 DIAVLQVQWERLNADLHEIPEVDMTRRLDITGLCGFNRYRNSFYRDQPHPTSMVRA 180  
 QY 181 LDEAMNKLQANPDDPAYDENRQFOEDIKVNDLVDKIADKASQESDILLTHMLNG 240  
 DB 181 LDEAMNKLQANPDDPAYDENRQFOEDIKVNDLVDKIADKASQESDILLTHMLNG 240  
 QY 241 KDPETGEPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLRKAAEAAARVLD 300  
 DB 241 KDPETGEPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLRKAAEAAARVLD 300  
 QY 301 PVPYSQVQKLVKGVNLNEALRLWTPAFSLYAKEDIVLGGEYPLEKGEDELVLIPOL 360  
 DB 301 PVPYSQVQKLVKGVNLNEALRLWTPAFSLYAKEDIVLGGEYPLEKGEDELVLIPOL 360  
 QY 361 HRDRTTWGDDVEFRPERENPSAIPQAFKPGNGQRACIGQOPALHEATLVLGWMLKH 420  
 DB 361 HRDRTTWGDDVEFRPERENPSAIPQAFKPGNGQRACIGQOPALHEATLVLGWMLKH 420  
 QY 421 FDPEDHTNYELDIKETLTKPEGVYVAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 480  
 DB 421 FDPEDHTNYELDIKETLTKPEGVYVAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 480  
 QY 481 PLLVLVYSGNMGTAEGTARDLADIAKSGFAPQVATLDHAGNLPRGAVLIVTASVNGHP 540  
 DB 481 PLLVLVYSGNMGTAEGTARDLADIAKSGFAPQVATLDHAGNLPRGAVLIVTASVNGHP 540  
 QY 541 PDNAKQFVDWLQASADEKGVYRVYVFGCGDKNWTYOKVAFIDETLAAGAENIADR 600  
 DB 541 PDNAKQFVDWLQASADEKGVYRVYVFGCGDKNWTYOKVAFIDETLAAGAENIADR 600  
 QY 601 GEADASDDPEGTYEWEHREHMSDVAAVFNLDIENSEDNKSTLSLQFVDSAAADMLAKMHG 660  
 DB 601 GEADASDDPEGTYEWEHREHMSDVAAVFNLDIENSEDNKSTLSLQFVDSAAADMLAKMHG 660  
 QY 661 AFSTNVVASKELQOPQSARSTRHELELPKEASQYQEGDHLGVIPRNYGIVNRVTRARFGL 720  
 DB 661 AFSTNVVASKELQOPQSARSTRHELELPKEASQYQEGDHLGVIPRNYGIVNRVTRARFGL 720  
 QY 721 DASQQLRLAEAEKLAHLPLAKTVSVVEELQVVELQDPVTRTQLRAMAAKTVCPPHKVEL 780  
 DB 721 DASQQLRLAEAEKLAHLPLAKTVSVVEELQVVELQDPVTRTQLRAMAAKTVCPPHKVEL 780

QY 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKFSFIALPSIRPRYKSISSPRVDEK 840  
 DB 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKFSFIALPSIRPRYKSISSPRVDEK 840  
 QY 841 QASITVSVYSGEAMSGYGYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900  
 DB 841 QASITVSVYSGEAMSGYGYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900  
 QY 901 VPGTGVAPFRGVQARKQKQKQSLGSAHLYFGCRSPHEDYLYQEELNAQSEGIITL 960  
 DB 901 VPGTGVAPFRGVQARKQKQKQSLGSAHLYFGCRSPHEDYLYQEELNAQSEGIITL 960  
 QY 961 HTAFSRMPNQPKTYVQHVMEQDQKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 DB 961 HTAFSRMPNQPKTYVQHVMEQDQKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 QY 1021 HOVSEADARLWLOOLEEKGRYAKDVWAG 1048  
 DB 1021 HOVSEADARLWLOOLEEKGRYAKDVWAG 1048

RESULT 2  
 AAB46855  
 ID AAB46855 standard; Protein; 1048 AA.  
 XX  
 AC AAB46855;  
 XX AC  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE B. megaterium cytochrome P450 monooxygenase BM-3 protein.  
 XX  
 KW Cytochrome P450 monooxygenase; BM-3; electron donor system; bioreactor;  
 KW electron transfer; hydroxylatable fatty acid; fatty acid-monooxygenase.  
 XX  
 OS Bacillus megaterium.  
 XX  
 PN WO200107573-A1.  
 PD  
 XX 01-FEB-2001.  
 XX  
 PF 27-JUL-2000; 2000WO-EP07251.  
 XX  
 PR 27-JUL-1999; 99DE-1035115.  
 PR 10-MAR-2000; 2000DE-1011723.  
 XX  
 PA (BADI ) BASF AG.  
 XX  
 PI Hauer B, Schmid RD, Schwaneberg U;  
 DR WPI; 2001-159709/16.  
 DR N-PSDB; AAF26268.  
 XX  
 PT Novel electron donor system useful for the production of  
 PT omega-hydroxylated fatty acids comprises an inorganic electron sink and  
 PT a mediator which enables the electron transfer -  
 XX  
 PS Claim 13b; Page 83-86; 94pp; German.  
 XX  
 CC This invention describes a novel electron donor system (M1) that  
 CC transfers electrons to an enzyme with redox properties comprising an  
 CC inorganic, not electrode-bound, electron sink and a mediator which enable  
 CC the electron transfer. The invention also describes (1) transferring (M2)  
 CC oxygen to a hydrocarbon containing hydrogen donor molecule, where the  
 CC hydrogen donor molecule is in a reaction medium comprising the oxygen  
 CC transferring enzyme and (M1) in the presence of oxygen and incubating  
 CC under suitable reaction conditions; (2) the enzymatic production (M3) of  
 CC terminally or subterminally hydroxylated (position omega-1 to omega-4)  
 CC fatty acids comprising: (i) mixing a hydroxylatable fatty acid or fatty  
 CC acid derivative in the presence of (M1) and cytochrome P450  
 CC monooxygenase; and (ii) isolating the hydroxylated product; (3) a  
 CC bioreactor useful for the production of omega-hydroxylated fatty acids as  
 CC described in (2); and (4) detecting (M4) fatty acid-monooxygenases  
 CC comprising: (1) contacting the analyte with a omega-hydroxylatable fatty

CC acid or a derivative comprising a terminal chromophore or fluorescent  
CC label in (M); and (ii) qualitatively or quantitatively detecting the  
CC signal. The invention is useful for the production of omega-hydroxylated  
CC fatty acids and the detection of fatty acid monooxygenases. The  
CC invention provides an alternative electron donor system of enzymes with  
CC redox properties that is cheaper and more efficient, where the enzyme  
CC comprises cytochrome 450.

XX  
SQ Sequence 1048 AA;

Query Match 100.0%; Score 5457; DB 22; Length 1048;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMQPKTFGELKPLILNTDKPVQALMKIADDELGEIFKFPAGRVTRYLSQRLIKE 60  
DB 1 TIKEMQPKTFGELKPLILNTDKPVQALMKIADDELGEIFKFPAGRVTRYLSQRLIKE 60

QY 61 ACDESFPDKNLSQALFVRDFAGDGLFTSWTHEKNMKKAHNILLPSFSQAMKGYHAMV 120  
DB 61 ACDESFPDKNLSQALFVRDFAGDGLFTSWTHEKNMKKAHNILLPSFSQAMKGYHAMV 120

QY 121 DIAVOLVQWERLNADHEIEVPEDMTRLTDLTGLCGFNFRFNSFYEDQPHPTITSMVRA 180  
DB 121 DIAVOLVQWERLNADHEIEVPEDMTRLTDLTGLCGFNFRFNSFYEDQPHPTITSMVRA 180

QY 181 LDEAMNKLRANPDPPAYDENKRFQFQEDIKVMNDLVDKIITADRKASGEQSDLLTHMLNG 240  
DB 181 LDEAMNKLRANPDPPAYDENKRFQFQEDIKVMNDLVDKIITADRKASGEQSDLLTHMLNG 240

QY 241 KDPETGEPLDDENIRYOITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEPAARVLD 300  
DB 241 KDPETGEPLDDENIRYOITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEPAARVLD 300

QY 301 PVPYSYQVKOLKYGVMVNEALRLWPTAPAFSLYAKEDTVILGGEYPLEKGDMLVLPQL 360  
DB 301 PVPYSYQVKOLKYGVMVNEALRLWPTAPAFSLYAKEDTVILGGEYPLEKGDMLVLPQL 360

QY 361 HRDKTIWGDDVEEFREPERFENPQAFKPFNGGRCIGQOFALHEATLVGLWMLKH 420  
DB 361 HRDKTIWGDDVEEFREPERFENPQAFKPFNGGRCIGQOFALHEATLVGLWMLKH 420

QY 421 FDFEDHTNYELDKETLTKPEGVVKAQSKKIPGLGIPSPSTEQSAKKVKKKAENAHNT 480  
DB 421 FDFEDHTNYELDKETLTKPEGVVKAQSKKIPGLGIPSPSTEQSAKKVKKKAENAHNT 480

QY 481 PLLVLVGSNMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540  
DB 481 PLLVLVGSNMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540

QY 541 PDNAKQFVWLQASADEVKGVRYSVFGCGDKNWTYQKVPFIDETLAAKGAENIADR 600  
DB 541 PDNAKQFVWLQASADEVKGVRYSVFGCGDKNWTYQKVPFIDETLAAKGAENIADR 600

QY 601 GEADASDDFGTVEEWHMWSVAAVFNLDIENSEDNKSTLSQFVDSAADPLAKMHG 660  
DB 601 GEADASDDFGTVEEWHMWSVAAVFNLDIENSEDNKSTLSQFVDSAADPLAKMHG 660

QY 661 AFSTNVVAKELQPGSARSSTRHLELPEKASVOEGDHLGVIPRNVGIVNRTAFGL 720  
DB 661 AFSTNVVAKELQPGSARSSTRHLELPEKASVOEGDHLGVIPRNVGIVNRTAFGL 720

QY 721 DASQIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAATVCPPHKVEL 780  
DB 721 DASQIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAATVCPPHKVEL 780

QY 781 EALLEKQAYEQVLAKRLTLMLELKYPCAKEMFSEFIALLPISRPRIYSSISPRVDEK 840  
DB 781 EALLEKQAYEQVLAKRLTLMLELKYPCAKEMFSEFIALLPISRPRIYSSISPRVDEK 840

QY 841 QASITVSVSGEAWSGYGEYKGTASNYLAELQEGDITTCISTPQSEFTLPKDPETPLIM 900  
DB 841 QASITVSVSGEAWSGYGEYKGTASNYLAELQEGDITTCISTPQSEFTLPKDPETPLIM 900

QY 901 VGPCTGVAPPRGFQARKQKLEQGSILGEAHLFGCRSPHEDYLYQELENAOSEGIITL 960  
DB 901 VGPCTGVAPPRGFQARKQKLEQGSILGEAHLFGCRSPHEDYLYQELENAOSEGIITL 960

QY 961 HTAFSRMPNQPRTYVQHVMBQDGKLLIELDQGAHFYICGDSQMAPAVATLMKSYADV 1020  
DB 961 HTAFSRMPNQPRTYVQHVMBQDGKLLIELDQGAHFYICGDSQMAPAVATLMKSYADV 1020

QY 1021 HQVSEADARLWLOOLEKGRYAKDVWAG 1048  
DB 1021 HQVSEADARLWLOOLEKGRYAKDVWAG 1048

RESULT 3  
AAB46856  
ID AAB46856 standard; Protein; 1048 AA.  
XX  
AC AAB46856;  
XX  
DT 02-MAY-2001 (first entry)  
XX  
DE B. megaterium cytochrome P450 monooxygenase BM-3 protein.  
XX  
KW Cytochrome P450 monooxygenase; BM-3; site-specific mutagenesis;  
KW aliphatic carboxylic acid hydroxylation; fatty acid.  
OS Bacillus megaterium.  
XX  
PN W0200107574-A2.  
PD 01-FEB-2001.  
PF 27-JUL-2000; 2000WO-EP07252.  
XX  
PR 27-JUL-1999; 99DE-1035115.  
PR 10-MAR-2000; 2000DE-1011723.  
XX  
PA (BADI ) BASF AG.  
PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;  
PI Li Q;  
DR WPI; 2001-159710/16.  
DR N-PSDB; AAF26324.  
XX  
PT New modified cytochrome P450 mono-oxygenase, useful for producing  
PT hydroxylated aliphatic carboxylic acids and derivatives, has altered  
PT substrate specificity -  
XX  
PS Claim 3; Page 41-45; 49pp; German.  
XX  
CC This invention describes a novel modified cytochrome P450 (I) having, as  
CC a result of site-specific mutagenesis of its substrate-binding domain,  
CC an altered substrate profile, relative to the wild-type, when used for  
CC terminal and/or subterminal enzymatic hydroxylation of aliphatic  
CC carboxylic acids. The invention also describes (i) nucleic acid (ii)  
CC encoding (i), and its complement; (2) expression cassette (EC) containing  
CC (ii) and control elements; (3) a vector containing at least one EC; (4)  
CC recombinant microorganisms transformed with at least one vector of (3);  
CC and (5) enzymatic production of terminally and/or subterminally  
CC hydroxylated aliphatic carboxylic acids (A) using the microorganisms of  
CC (4), or isolated (i). (i), and recombinant cells that express them, are  
CC used to produce hydroxylated aliphatic carboxylic acids or their  
CC derivatives (esters and amides). (i) have altered substrate specificity,  
CC especially for hydroxylation of 8-12C fatty acids at the omega-1, -2  
CC and/or -3 positions, and may also have increased reactivity and/or  
CC regioselectivity.  
SQ Sequence 1048 AA;

Query Match 100.0%; Score 5457; DB 22; Length 1048;  
Best Local Similarity 100.0%; Pred. No. 0;





Db 122 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFSFYRDPHPFITSMVRA 181  
Qy 181 LDEAMNKLQANPPDPAYDENKROFQEDIKVMDLVDKIIADRKASQSDLLTHMLNG 240  
Db 182 LDEAMNKLQANPPDPAYDENKROFQEDIKVMDLVDKIIADRKASQSDLLTHMLNG 241  
Qy 241 KDPETGPELDDENIRYQIITFLIAGHETTGLLSFALYFLVKNPHVLQKAAEAAARLVLD 300  
Db 242 KDPETGPELDDENIRYQIITFLIAGHETTGLLSFALYFLVKNPHVLQKAAEAAARLVLD 301  
Qy 301 PVPYSKOVKOLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGYPLEKGDLMVLIPOL 360  
Db 302 PVPYSKOVKOLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGYPLEKGDLMVLIPOL 361  
Qy 361 HRDKTIWGDVVEEPRPERFENPSAIPQHAFFPGNGQACIGQFALHEATVLVGMMLKH 420  
Db 362 HRDKTIWGDVVEEPRPERFENPSAIPQHAFFPGNGQACIGQFALHEATVLVGMMLKH 421  
Qy 421 FDFEDHTNYELDIKETITLTKPEGFVVKAKSKKIPGLGIPSPSTEQSAKKVRKKAENAHT 480  
Db 422 FDFEDHTNYELDIKETITLTKPEGFVVKAKSKKIPGLGIPSPSTEQSAKKVRKKAENAHT 481  
Qy 481 PLLVLYGSNMGTAGTARDLADIAMSGFAPOVATLDSHAGNLPREGAVLIVTASYNGHP 540  
Db 482 PLLVLYGSNMGTAGTARDLADIAMSGFAPOVATLDSHAGNLPREGAVLIVTASYNGHP 541  
Qy 541 PDNAKQFVMDLQASADEVKGVRYSVFCGDKNWTYQKVPAPFIDETLAAKGAENIADR 600  
Db 542 PDNAKQFVMDLQASADEVKGVRYSVFCGDKNWTYQKVPAPFIDETLAAKGAENIADR 601  
Qy 601 GEADASDDFEGTYEWEHMHMSDVAAYFNLDIENSDNKSTLSLQFVDSAADMPLAKMHG 660  
Db 602 GEADASDDFEGTYEWEHMHMSDVAAYFNLDIENSDNKSTLSLQFVDSAADMPLAKMHG 661  
Qy 661 AFSTNVVASKELQPGSARSSTRHLEIELPREASTQEGDHLGVIPRNYEGIVNRYTAREGL 720  
Db 662 AFSTNVVASKELQPGSARSSTRHLEIELPREASTQEGDHLGVIPRNYEGIVNRYTAREGL 721  
Qy 721 DASQOIRLEAEEKLAHLPLAKTVSVELLQYVLELQDPVTRTQLRAMAAKTVCPPHKVEL 780  
Db 722 DASQOIRLEAEEKLAHLPLAKTVSVELLQYVLELQDPVTRTQLRAMAAKTVCPPHKVEL 781  
Qy 781 EALLEKQAYKEQVLAKRLTLMLELLEKYPACEMKSEFIALPLSPRPRYSISSSPRYDEK 840  
Db 782 EALLEKQAYKEQVLAKRLTLMLELLEKYPACEMKSEFIALPLSPRPRYSISSSPRYDEK 841  
Qy 841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900  
Db 842 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 901  
Qy 901 VPGTGVAPFRGFVQARKQLKEQOSLGEAHLFYGCRSPHEDYLYQBELENAQSEGITL 960  
Db 902 VPGTGVAPFRGFVQARKQLKEQOSLGEAHLFYGCRSPHEDYLYQBELENAQSEGITL 961  
Qy 961 HTAFSRPNQPTVQHVMEODGKKLIELLDQGAHFYICGDSQMAVAEATLMKSYADV 1020  
Db 962 HTAFSRPNQPTVQHVMEODGKKLIELLDQGAHFYICGDSQMAVAEATLMKSYADV 1021  
Qy 1021 HQVSEADARLWLOOLEKGRYAKDVWAG 1048  
Db 1022 HQVSEADARLWLOOLEKGRYAKDVWAG 1049

RESULT 5

AAB31882

ID AAB31882 standard; Protein; 1049 AA.

XX AAB31882;

DT 15-MAY-2001 (first entry)

DE Amino acid sequence of a Bacillus P450 monooxygenase protein.

XX

KW Cytochrome P450 monooxygenase; oxidization; indole; indigo; indorubicin.  
XX Bacillus megaterium.  
OS WO200107630-A1.  
PN 01-FEB-2001.  
PD 27-JUL-2000; 2000WO-EP07253.  
PF 27-JUL-1999; 99DE-10351115.  
PR 18-NOV-1999; 99DE-1055605.  
PR 22-MAR-2000; 2000DE-1014085.  
XX (BADI ) BASF AG.  
XX Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;  
PI Li Q;  
XX WPI; 2001-182800/18.  
DR Cytochrome P450 monooxygenase for oxidizing organic compounds, useful  
XX especially for converting indole to indigo, has wide substrate range -  
PT Disclosure; Page 41-44; 54pp; German.  
PS The present sequence represents a cytochrome P450 monooxygenase. The  
XX specification describes a modified cytochrome P450 monooxygenase which  
CC can oxidize at least one of the following types of substrates:  
CC optionally substituted mono- or poly-cyclic aromatic heterocyclics  
CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or  
CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or  
CC optionally substituted cycloalkanes or cycloalkenes. The modified  
CC cytochrome P450 monooxygenase are specifically used to oxidize indole  
CC to indigo and indorubicin. However, they may be used to oxidise many  
CC other substrates.  
XX  
SQ Sequence 1049 AA;  
Query Match 100.0%; Score 5457; DB 22; Length 1049;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TIKEMPOKPTGELKNLPLNTDKPVQALMKIADLGEIFKEAPGRVTRVYLSORLIKE 60  
Db 2 TIKEMPOKPTGELKNLPLNTDKPVQALMKIADLGEIFKEAPGRVTRVYLSORLIKE 61  
Qy 61 ACDESREDKNSQALKFVRDFAGDGLFTSWTHEKNWKAHNLILPFSQQAAMGYHAMV 120  
Db 62 ACDESREDKNSQALKFVRDFAGDGLFTSWTHEKNWKAHNLILPFSQQAAMGYHAMV 121  
Qy 121 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFSFYRDPHPFITSMVRA 180  
Db 122 DIAVOLQVQWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFSFYRDPHPFITSMVRA 181  
Qy 181 LDEAMNKLQANPPDPAYDENKROFQEDIKVMDLVDKIIADRKASQSDLLTHMLNG 240  
Db 182 LDEAMNKLQANPPDPAYDENKROFQEDIKVMDLVDKIIADRKASQSDLLTHMLNG 241  
Qy 241 KDPETGPELDDENIRYQIITFLIAGHETTGLLSFALYFLVKNPHVLQKAAEAAARLVLD 300  
Db 242 KDPETGPELDDENIRYQIITFLIAGHETTGLLSFALYFLVKNPHVLQKAAEAAARLVLD 301  
Qy 301 PVPYSKOVKOLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGYPLEKGDLMVLIPOL 360  
Db 302 PVPYSKOVKOLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGYPLEKGDLMVLIPOL 361  
Qy 361 HRDKTIWGDVVEEPRPERFENPSAIPQHAFFPGNGQACIGQFALHEATVLVGMMLKH 420  
Db 362 HRDKTIWGDVVEEPRPERFENPSAIPQHAFFPGNGQACIGQFALHEATVLVGMMLKH 421  
Qy 421 FDFEDHTNYELDIKETITLTKPEGFVVKAKSKKIPGLGIPSPSTEQSAKKVRKKAENAHT 480

Db 422 DFDHTNYELDIKETITLTKPEGVVKAKSKKIPGLGIPSPSTEQSAKKVRKAENAHT 481  
QY 481 PLLVLYGSMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 540  
Db 482 PLLVLYGSMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 541  
QY 541 PDNAKQFVMDLQASADEVKGVYRVYFGCGDKNWTYYQKVPFIDETLAAKGAENIADR 600  
Db 542 PDNAKQFVMDLQASADEVKGVYRVYFGCGDKNWTYYQKVPFIDETLAAKGAENIADR 601  
QY 601 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 660  
Db 602 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 661  
QY 661 AFSTNVVASKELQOPGASRSTRHLELELPKEASYQEGDHLGVIPRNYEGIVNRVARTFGL 720  
Db 662 AFSTNVVASKELQOPGASRSTRHLELELPKEASYQEGDHLGVIPRNYEGIVNRVARTFGL 721  
QY 721 DASQQLRLEAEKEKLAHLPLAKTVSVEELIQVVELOQVDPVTRTQLRAMAAKTVCPPHKVEL 780  
Db 722 DASQQLRLEAEKEKLAHLPLAKTVSVEELIQVVELOQVDPVTRTQLRAMAAKTVCPPHKVEL 781  
QY 781 EALLEKQAYKEQVLAKRLTMELELKYIPACEMKFSEFIALLPSPRYYISISSPRVDEK 840  
Db 782 EALLEKQAYKEQVLAKRLTMELELKYIPACEMKFSEFIALLPSPRYYISISSPRVDEK 841  
QY 841 QASITVSVYGSAWSGYGYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900  
Db 842 QASITVSVYGSAWSGYGYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 901  
QY 901 VGPGTGVPFGRFVQARKOLKEQGSGLGBAHLFGCRSPHEDYLYQEELENAQSEGIITL 960  
Db 902 VGPGTGVPFGRFVQARKOLKEQGSGLGBAHLFGCRSPHEDYLYQEELENAQSEGIITL 961  
QY 961 HTAFSRMPNPKTYVQHVMEQDGKLIIELLDQGAHEYICGDSQMAPAVEATLMKSYADY 1020  
Db 962 HTAFSRMPNPKTYVQHVMEQDGKLIIELLDQGAHEYICGDSQMAPAVEATLMKSYADY 1021  
QY 1021 HOVSEADARLWLQOLEKGRYAKDVWAG 1048  
Db 1022 HOVSEADARLWLQOLEKGRYAKDVWAG 1049

## RESULT 6

AAB31979

ID AAB31979 standard; Protein; 1048 AA.

XX

AC AAB31979;

XX

DT 15-MAY-2001 (first entry)

XX

DE Amino acid sequence of a modified P450 monooxygenase protein.

XX

KW Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.

XX

OS Bacillus megaterium.

XX

FH Key Location/Qualifiers

FT Misc-difference 87

FT /note= "wild type Phe changed to Val."

XX

PN WO200107630-A1.

XX

PD 01-FEB-2001.

XX

PF 27-JUL-2000; 2000WO-BP07253.

XX

PR 27-JUL-1999; 99DE-1035115.

XX

PR 18-NOV-1999; 99DE-1055605.

XX

PR 22-MAR-2000; 2000DE-1014085.

XX

PA (BADI ) BASF AG.

XX

PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;  
PI Li Q;  
XX WPI; 2001-182800/18.  
DR  
XX  
PT Cytochrome P450 monooxygenase for oxidizing organic compounds, useful  
especially for converting indole to indigo, has wide substrate range -  
XX  
PS Claim 5; Page -; 54pp; German.

The present sequence represents a modified cytochrome P450 monooxygenase.  
The specification describes a modified cytochrome P450 monooxygenase  
which can oxidize at least one of the following types of substrates:  
CC optionally substituted mono- or poly-cyclic aromatic heterocyclics  
CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or  
CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or  
CC optionally substituted cycloalkanes or cycloalkenes. The modified  
CC cytochrome P450 monooxygenase are specifically used to oxidize indole  
CC to indigo and indorubicin. However, they may be used to oxidise many  
CC other substrates.  
CC note: this sequence does not appear in the specification; it was created  
CC using information provided.

XX Sequence 1048 AA;

Query Match 99.9%; Score 5450; DB 22; Length 1048;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1047; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTKEMPQPKTFGELKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSORLIKE 60  
Db 1 TTKEMPQPKTFGELKNLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSORLIKE 60  
QY 61 ACDESREFDKNLQALKFVDFAGDGLFTSWTHEKNWKAHNILLFSQOAMKGYHAMV 120  
Db 61 ACDESREFDKNLQALKFVDFAGDGLFTSWTHEKNWKAHNILLFSQOAMKGYHAMV 120  
QY 121 DIAVLQVKWERLNDAHEIEVPEDMTRLTLDITGLCGFNRYNSFYRQPHFITSMVRA 180  
Db 121 DIAVLQVKWERLNDAHEIEVPEDMTRLTLDITGLCGFNRYNSFYRQPHFITSMVRA 180  
QY 181 LDEAMNKLQANPPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG 240  
Db 181 LDEAMNKLQANPPDDPAYDENKRFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG 240  
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPVLQAAEAAARLVLD 300  
Db 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPVLQAAEAAARLVLD 300  
QY 301 PVPSYKQVKQLKYGVMVNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELVLIPOL 360  
Db 301 PVPSYKQVKQLKYGVMVNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELVLIPOL 360  
QY 361 HRDKTIWGDVDEFFRPERFENPSPAIPQHAFFKFGNGQACICQQFALHATVILGNMLKH 420  
Db 361 HRDKTIWGDVDEFFRPERFENPSPAIPQHAFFKFGNGQACICQQFALHATVILGNMLKH 420  
QY 421 DFDHTNYELDIKETITLTKPEGVVKAKSKKIPGLGIPSPSTEQSAKKVRKAENAHT 480  
Db 421 DFDHTNYELDIKETITLTKPEGVVKAKSKKIPGLGIPSPSTEQSAKKVRKAENAHT 480  
QY 481 PLLVLYGSMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 540  
Db 481 PLLVLYGSMGTAEGTARDLADTAMSGFAPQVATLDSHAGNLPREGAVLIIVTASNGHP 540  
QY 541 PDNAKQFVMDLQASADEVKGVYRVYFGCGDKNWTYYQKVPFIDETLAAKGAENIADR 600  
Db 541 PDNAKQFVMDLQASADEVKGVYRVYFGCGDKNWTYYQKVPFIDETLAAKGAENIADR 600  
QY 601 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 660  
Db 601 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 660

661	QY	AFSTNVVASKELQOQPGSARSTRHLEITELPKESYQEGDHLGVIPRNYEGIVNRVTA	RFL	720
661	Db	AFSTNVVASKELQOQPGSARSTRHLEITELPKESYQEGDHLGVIPRNYEGIVNRVTA	RFL	720
721	QY	DASQQIRLRAEEKLAHLPLAKTVSVEELLQVYVELODPVTRQLRMAAKTVCP	PHKVEL	780
721	Db	DASQQIRLRAEEKLAHLPLAKTVSVEELLQVYVELODPVTRQLRMAAKTVCP	PHKVEL	780
781	QY	EALLERQAYKEQVIAKRLTMELELKYPCACMKFSEFIALLPSIRPRYSISS	SPRVDEK	840
781	Db	EALLERQAYKEQVIAKRLTMELELKYPCACMKFSEFIALLPSIRPRYSISS	SPRVDEK	840
841	QY	QASITVSVVSGEAWSGYGEYKGIASNYLAELQBGDITCFISTPQSEFTLP	KDPETPLIM	900
841	Db	QASITVSVVSGEAWSGYGEYKGIASNYLAELQBGDITCFISTPQSEFTLP	KDPETPLIM	900
901	QY	VGPCTGVAPFRGVQARKOLKEQGQSIGBAHLVFGCRSPHEDLYLOEELNAQ	SEGIITL	960
901	Db	VGPCTGVAPFRGVQARKOLKEQGQSIGBAHLVFGCRSPHEDLYLOEELNAQ	SEGIITL	960
961	QY	HTAFSRMPNQPTYTVQHVMEQDGKLIETLDDQGAHFYICDGSQMAPAVEAT	LKMSYADV	1020
961	Db	HTAFSRMPNQPTYTVQHVMEQDGKLIETLDDQGAHFYICDGSQMAPAVEAT	LKMSYADV	1020
1021	QY	HQVSEADARLWLOOLEEKGRYAKDVWAG	1048	
1021	Db	HQVSEADARLWLOOLEEKGRYAKDVWAG	1048	

## RESULT 7

AA	AY72208
ID	AA Y72208 standard; Protein; 1049 AA.
XX	
AC	AA Y72208;
XX	
DT	24-APR-2001 (first entry)
XX	
DE	Bacillus megaterium monooxygenase enzyme homologue, P450BM-3.
XX	
KW	Monooxygenase enzyme; P450BM-3 homologue; P450cam; oxidation;
KW	halogenated aromatic compound; electron transfer; putidaredoxin;
KW	putidaredoxin reductase; detoxification.
XX	
OS	Bacillus megaterium.
XX	
PN	WO200078973-A1.
XX	
PD	28-DEC-2000.
XX	
PF	19-JUN-2000; 2000WO-CB02379.
XX	
PR	18-JUN-1999; 99GB-0014373.
XX	
PA	(ISIS-) ISIS INNOVATION LTD.
XX	
PI	Wong LL, Jones JP;
XX	
DR	WPI; 2001-071397/08.
DR	N-PSDB; AAD02365.
PT	New process for detoxifying environments contaminated with halo
XX	aromatic compounds comprises treating the affected area with a
PT	monooxygenase enzyme.
XX	
PS	Disclosure; Page 32-39; 42pp; English.
XX	
CC	The present invention relates to a process for enzymatically oxidising
CC	the halogenated aromatic compounds such as 1,2-dichlorobenzene,
CC	1,2,4-trichlorobenzene, 3,3'-dichlorobiphenyl or 2,2',4,5,
CC	5-pentachlorobiphenyl. The process comprises treating the polluted
CC	environment with a monooxygenase enzyme. A monooxygenase enzyme, P450cam,
CC	and its physiological electron transfer partners, putidaredoxin and
CC	putidaredoxin reductase, are used to oxidise the halogenated aromatic

QY 901 VPGGTGVPFRGFVQARKQKQSGSLGEAHLFGCRSPHEDYLYQEELENAQSGIITL 960  
 DB 902 VPGGTGVPFRGFVQARKQKQSGSLGEAHLFGCRSPHEDYLYQEELENAQSGIITL 961  
 QY 961 HTAFSRMPNPKTYVQHVMEQDQKGLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 DB 962 HTAFSRMPNPKTYVQHVMEQDQKGLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021  
 QY 1021 HQVSEADARLWLQOLEEKGRYAKDWWAG 1048  
 DB 1022 HQVSEADARLWLQOLEEKGRYAKDWWAG 1049

RESULT 8  
 ID AAB31980 standard; Protein; 1048 AA.  
 XX  
 AC AAB31980;  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Amino acid sequence of a modified P450 monooxygenase protein.  
 XX  
 KW Cytochrome P450 monooxygenase; oxidization; indole; indigo; indorubicin.  
 OS Bacillus megaterium.  
 FH Key Location/Qualifiers  
 FT Misc-difference 87 /note= "wild type Phe changed to Val"  
 FT Misc-difference 188 /note= "wild type Leu changed to Gln"  
 FT  
 XX  
 PN WO200107630-A1.  
 XX  
 PD 01-FEB-2001.  
 XX  
 PF 27-JUL-2000; 2000WO-BP07253.  
 PR 27-JUL-1999; 99DE-1035115.  
 PR 18-NOV-1999; 99DE-1055605.  
 PR 22-MAR-2000; 2000DE-1014085.  
 XX  
 PA (BADI ) BASF AG.  
 XX  
 PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;  
 PI Li Q;  
 XX  
 DR WPI: 2001-182800/18.  
 XX  
 PT Cytochrome P450 monooxygenase for oxidizing organic compounds, useful  
 PT especially for converting indole to indigo, has wide substrate range -  
 XX  
 PS Claim 5; Page -: 54pp; German.  
 XX  
 CC The present sequence represents a modified cytochrome P450 monooxygenase.  
 CC The specification describes a modified cytochrome P450 monooxygenase  
 CC which can oxidize at least one of the following types of substrates:  
 CC optionally substituted mono- or poly-cyclic aromatic heterocyclics  
 CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or  
 CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or  
 CC optionally substituted cycloalkanes or cycloalkenes. The modified  
 CC cytochrome P450 monooxygenase are specifically used to oxidize indole  
 CC to indigo and indorubicin. However, they may be used to oxidise many  
 CC other substrates.  
 CC note: this sequence does not appear in the specification; it was created  
 CC using information provided.  
 XX  
 SQ Sequence 1048 AA;

Query Match 99.8%; Score 5444; DB 22; Length 1048;  
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TIKEMPOKTKGELKNLPLNTDKPQALMTADELGEIFKEAPGRVTRYLSSORLIKE 60  
 DB 1 TIKEMPOKTKGELKNLPLNTDKPQALMTADELGEIFKEAPGRVTRYLSSORLIKE 60  
 QY 61 ACDESFRDNISQALKFVRDFAGDGLFTSWTHEKNWKAHNLLPSFSQQAQMGYHAMV 120  
 DB 61 ACDESFRDNISQALKFVRDFAGDGLFTSWTHEKNWKAHNLLPSFSQQAQMGYHAMV 120  
 QY 121 DIAVOLVKWERLNADHEIEVPEDMTRTLDTIGLCGFNRYNSFYRQPHFITSMVRA 180  
 DB 121 DIAVOLVKWERLNADHEIEVPEDMTRTLDTIGLCGFNRYNSFYRQPHFITSMVRA 180  
 QY 181 LDEAMNKLQRANPPDDPAYDENKRFQEDIKVMNDLVDKTIADRKASGSDLLTHMLNG 240  
 DB 181 LDEAMNKLQRANPPDDPAYDENKRFQEDIKVMNDLVDKTIADRKASGSDLLTHMLNG 240  
 QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLD 300  
 DB 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLD 300  
 QY 301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELAVLIQOL 360  
 DB 301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELAVLIQOL 360  
 QY 361 HRDKTIWGDVDEEFPERFENPSAIPQHAFKPFNGQACIGQQFALHEATLVLMMLKH 420  
 DB 361 HRDKTIWGDVDEEFPERFENPSAIPQHAFKPFNGQACIGQQFALHEATLVLMMLKH 420  
 QY 421 FDFEDHTNYELDIKETLTKPEGFVVKAKSKIPGIGIPSPSTESAKVRKKAENAHNT 480  
 DB 421 FDFEDHTNYELDIKETLTKPEGFVVKAKSKIPGIGIPSPSTESAKVRKKAENAHNT 480  
 QY 481 PLLVLYGSGNMGTAEGTARDLADIAAMSKGFAPQVATLDSHAGNLREGAVLIVTASYNCHP 540  
 DB 481 PLLVLYGSGNMGTAEGTARDLADIAAMSKGFAPQVATLDSHAGNLREGAVLIVTASYNCHP 540  
 QY 541 PDNAKQFVDLQDQASADEVKGVYRVFVCGDKNWTATYQKVPFIDETLAAGAENIADR 600  
 DB 541 PDNAKQFVDLQDQASADEVKGVYRVFVCGDKNWTATYQKVPFIDETLAAGAENIADR 600  
 QY 601 GEADASDDFEGTYEWRHMHMSDVAAYFNLDIENSEDNKSTLSLQFVDSADMPKAKMHG 660  
 DB 601 GEADASDDFEGTYEWRHMHMSDVAAYFNLDIENSEDNKSTLSLQFVDSADMPKAKMHG 660  
 QY 661 AFSTNVVASKELQOPGSGARSTRHLIELPKEASYQEGDHLGVIIPRYEGIVNRVTARFGL 720  
 DB 661 AFSTNVVASKELQOPGSGARSTRHLIELPKEASYQEGDHLGVIIPRYEGIVNRVTARFGL 720  
 QY 721 DASQOIRLEAEERKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780  
 DB 721 DASQOIRLEAEERKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780  
 QY 781 EALLEKQAYKEQVLAKRLTLMLELLKYPACEMKFEFTALLPSIRPRYSISSSRVDEK 840  
 DB 781 EALLEKQAYKEQVLAKRLTLMLELLKYPACEMKFEFTALLPSIRPRYSISSSRVDEK 840  
 QY 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900  
 DB 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900  
 QY 901 VPGGTGVPFRGFVQARKQKQSGSLGEAHLFGCRSPHEDYLYQEELENAQSGIITL 960  
 DB 901 VPGGTGVPFRGFVQARKQKQSGSLGEAHLFGCRSPHEDYLYQEELENAQSGIITL 960  
 QY 961 HTAFSRMPNPKTYVQHVMEQDQKGLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 DB 961 HTAFSRMPNPKTYVQHVMEQDQKGLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 QY 1021 HQVSEADARLWLQOLEEKGRYAKDWWAG 1048  
 DB 1021 HQVSEADARLWLQOLEEKGRYAKDWWAG 1048

## RESULT 9

AAB31981  
ID AAB31981 standard; Protein; 1048 AA.

XX AC AAB31981;  
XX 15-MAY-2001 (first entry)

DT Amino acid sequence of a modified P450 monooxygenase protein.

DE Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.

XX OS Bacillus megaterium.

XX FH Key Location/Qualifiers

FT Misc-difference 74 /note= "wild type Ala changed to Gly"

FT Misc-difference 87 /note= "wild type Phe changed to Val"

FT Misc-difference 188 /note= "wild type Leu changed to Gln"

XX WO200107630-A1.

XX 01-FEB-2001.

XX 27-JUL-2000; 2000WO-EP07253.

XX 18-NOV-1999; 99DE-1035115.

XX 22-MAR-2000; 2000DE-1014085.

XX (BADI ) BASF AG.

XX Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;  
XX Li Q;

XX WPI; 2001-182800/18.

XX Cytochrome P450 monooxygenase for oxidizing organic compounds, useful  
XX especially for converting indole to indigo, has wide substrate range -

XX Claim 5; Page -: 54pp; German.

XX The present sequence represents a modified cytochrome P450 monooxygenase.

XX The specification describes a modified cytochrome P450 monooxygenase

XX which can oxidize at least one of the following types of substrates:

XX optionally substituted mono- or poly-cyclic aromatic heterocyclics

XX containing nitrogen, sulphur or oxygen; optionally substituted mono- or

XX poly-cyclic aromatics; linear or branched alkanes or alkenes; or

XX optionally substituted cycloalkanes or cycloalkenes. The modified

XX cytochrome P450 monooxygenase are specifically used to oxidize indole

XX to indigo and indorubicin. However, they may be used to oxidise many

XX other substrates.

XX note: this sequence does not appear in the specification; it was created

XX using information provided.

XX Sequence 1048 AA;

Query Match 99.7%; Score 5440; DB 22; Length 1048;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1045; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TIKEMPQKTFGEKLNPLNTDKPQALMKIADELGEIFKFEAPGRVTRYLSSORLIKE 60  
Db 1 TIKEMPQKTFGEKLNPLNTDKPQALMKIADELGEIFKFEAPGRVTRYLSSORLIKE 60

QY 61 ACDESREDKLSQALKEFVRDFAGDGLFTSWTHKKNKKAHNILLPSFSQAMKGYHAMV 120  
Db 61 ACDESREDKLSQALKEFVRDFAGDGLFTSWTHKKNKKAHNILLPSFSQAMKGYHAMV 120

QY 121 DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRNSFYRDQPHPTITSMVRA 180  
Db 121 DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRNSFYRDQPHPTITSMVRA 180  
QY 181 LDEAMNKLORANPDDPAYDENKRFQFEDIKVMNDLVKIIADRKASGEQSDLLTHMLNG 240  
Db 181 LDEAMNKLORANPDDPAYDENKRFQFEDIKVMNDLVKIIADRKASGEQSDLLTHMLNG 240  
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAARVLVD 300  
Db 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAARVLVD 300  
QY 301 PVPSYQVKOLKYVGMVNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLPOL 360  
Db 301 PVPSYQVKOLKYVGMVNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLPOL 360  
QY 361 HRDKTIWGGDDVEEPRPERFENPSAIPQHAFFKPGNGORACIGQOFALHEATLVGLMMLKH 420  
Db 361 HRDKTIWGGDDVEEPRPERFENPSAIPQHAFFKPGNGORACIGQOFALHEATLVGLMMLKH 420  
QY 421 FDFEDHTNYELDIKETITLTKPEGFVVKAKSKKIPLGIPSPSTEQSAKKVKKRAENAHT 480  
Db 421 FDFEDHTNYELDIKETITLTKPEGFVVKAKSKKIPLGIPSPSTEQSAKKVKKRAENAHT 480  
QY 481 PLLVLYGSNMGTAEGTARDLADIAMSGFAPOVATLDSHAGNLPRREGAVLIVTASYNGHP 540  
Db 481 PLLVLYGSNMGTAEGTARDLADIAMSGFAPOVATLDSHAGNLPRREGAVLIVTASYNGHP 540  
QY 541 PDNAKQFVMDLQASADEVKGVYRVGCGDKNWTYQKPAFIDFTLAAGAENADR 600  
Db 541 PDNAKQFVMDLQASADEVKGVYRVGCGDKNWTYQKPAFIDFTLAAGAENADR 600  
QY 601 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLOFVDSADMPKAKWHG 660  
Db 601 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLOFVDSADMPKAKWHG 660  
QY 661 AFSTNVVASKELQPGSARSSTRHLEIELPKEASYQEGDHLGVIIPRNYEGIVNVRTARFGL 720  
Db 661 AFSTNVVASKELQPGSARSSTRHLEIELPKEASYQEGDHLGVIIPRNYEGIVNVRTARFGL 720  
QY 721 DASQQIRLEAEKEKLAHLPLAKTVSVBELLOYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780  
Db 721 DASQQIRLEAEKEKLAHLPLAKTVSVBELLOYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780  
QY 781 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALPSIRPRYYSISSPRVDEK 840  
Db 781 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALPSIRPRYYSISSPRVDEK 840  
QY 841 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900  
Db 841 QASITVSVSGEAWSGYGYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900  
QY 901 VGPCTGVAPRGFVQARKQLKEQOSLGEAHLFGCSPHEDYLYQELENAQSEGITL 960  
Db 901 VGPCTGVAPRGFVQARKQLKEQOSLGEAHLFGCSPHEDYLYQELENAQSEGITL 960  
QY 961 HTAFSRMPNPKYVYVQHVMEQDKKLELDDOGAHHFYICGDSQMAPAVETLKMYSADV 1020  
Db 961 HTAFSRMPNPKYVYVQHVMEQDKKLELDDOGAHHFYICGDSQMAPAVETLKMYSADV 1020  
QY 1021 HOYSEADARLWLOOLEEKGRYAKDVWAG 1048  
Db 1021 HOYSEADARLWLOOLEEKGRYAKDVWAG 1048  
RESULT 10  
AAR11604  
ID AAR11604 standard; Protein; 1085 AA.  
XX AAR11604;  
AC AAR11604;  
XX 20-JUN-1991 (first entry)  
DT 20-JUN-1991 (first entry)  
XX

DE P450 17-alpha/p450 BM-3 fusion protein.  
 XX bovine adrenal; cytochrome P450; oxidase; reductase; steroid;  
 KW plasmid p(alphaBm1).  
 XX JP03061490-A.  
 XX 18-MAR-1991.  
 XX 28-JUL-1989; 89JP-0197296.  
 XX 28-JUL-1989; 89JP-0197296.  
 XX (SUMO ) SUMITOMO CHEM IND KK.  
 XX WPI; 1991-121848/17.  
 XX N-PSDB; AAQ11474.  
 XX P450 reductase fused oxidase coding gene - has both mono-atomic  
 PT oxygenation activity of bovine adrenal cytochrome p450 17-alpha  
 PT and reductivity supplying activity  
 XX Claim 1; Fig 2; 8pp; Japanese.  
 XX The protein is a fusion of bovine adrenal cytochrome P450 17-alpha  
 CC and Bacillus megaterium-derived cytochrome P450 BM-3. The fusion  
 CC protein has the monoatomic oxygenation activity of the former and  
 CC the reductivity supplying activity of the latter. plasmid p(alphaBm1),  
 CC containing the recombinant sequence encoding the fusion protein, is  
 CC used to transform Saccharomyces cerevisiae. The transformant is  
 CC designated AH22(p(alphaBm-1)) and can be used for the synthesis of  
 CC steroids.  
 XX Sequence 1085 AA;  
 SQ  
 Query Match 57.8%; Score 3154.5; DB 12; Length 1085;  
 Best Local Similarity 60.9%; Pred. No. 1.2e-211;  
 Matches 672; Conservative 105; Mismatches 222; Indels 105; Gaps 21;  
 QY 3 KEMPOKTEGKLNPLNTDTPVQALMKIADLGEIFKEAPGRVTRVLSQRLIKAC 62  
 DB RSLPSLVGLSLPFLP--RAGQHKNFQKLEKGYPIYSFRLGSKTVMIGHQLAREV- 85  
 QY 63 DESRFDKNSQALKFVRDPAG-----DGLFTSWTHKKNKMAHNLPSFS 108  
 DB 86 -----LLKKGKESGRPKVATLDILSDNKGIAFA-DHGAHWLHRKALNAFA 133  
 QY 109 QQAMKGYHAMVDIAVLQVKWERLNADEH---IEVPEDMTRLTLDITCLGCFNFSF 165  
 DB 134 --LFDGDNLUKEKIINQEANVLCDFLATQHGGAIDLSEPLSLAVTNLIISFCNFESFN- 190  
 QY 166 YRDQPHFTSMVRALDEAMNKLQANPDPPAYDENKQFQEDI----- 209  
 DB 191 -----EDPALKAQNVN--DGILEVLSKEVLDDIFVLKIPPSKAMEKMK 233  
 QY 210 ---KYVNDLVKIIADRRASGQSDLLTHMLN-----GKDPETGEPDLDENI---RY 256  
 DB 234 GCVOTRNELLNELL--EKOENFSDSITNLLHILIOAKVNADNNNAGPDQDQSKLLSNR 291  
 QY 257 QLIIT---FLIAGHETTSGLSLFALYFLVKNPHVLQKAAEAARVL-VDPVPSYKQVKLK 312  
 DB 292 MLIATIGDIFGAGVETTSVIRKIVAYLLHHPHSLKRRIQDDIQIIGFNRTPTISDRNLV 351  
 QY 313 YVGWLVNEALRWLPAPAFSLY-AKEDTVLGGYPLEKGEDELMVLIPQLHRDKTIWGDV 371  
 DB 352 LLEATIREVLRLRPVAPTLIPKAVIDSSI-GDLTIDKGTDDVVMWALHSEKEM-OHP 409  
 QY 372 EEFREPERENPSAI-----POHAFKPFNGQACIQQFALHEATLVLMGMLKHDFE--- 424  
 DB 410 DLFMPERFLDPTGTQLISPSLSYLPFGAGPRSCVGMELARQBELFLFMSRLQLQFNLEIPD 469  
 QY 425 DHTNVELDIKFTLLKPGCFVVKAKSKKIPGLGIPSPTEQSAKKVKRKAENAHNTPLLV 484

DB 470 DKLPSLEGHASLVLIQIKPFVKIEVRQ-----AWKEAQAGSTPCTAENAHNTPLLV 522  
 QY 485 LYGSNMGTAGETARDLADITAMSGFAPQVATLDSHAGNLPREGAVLIIVTASVNGHPPDNA 544  
 DB 523 LYGSNMGTAGETARDLADITAMSGFAPQVATLDSHAGNLPREGAVLIIVTASVNGHPPDNA 582  
 QY 545 KQFVDWLDAQSADEVKGVYRYSVFGCGDKNWNATTYQKVPAPAFIDETLAAKGAENIADRG 604  
 DB 583 KQFVDWLDAQSADEVKGVYRYSVFGCGDKNWNATTYQKVPAPAFIDETLAAKGAENIADRG 642  
 QY 605 ASDDFEGTYEWEHMSDVAAYFNLDIENSDNKSTLSLQFVDSAADMPLAKMHGAFST 664  
 DB 643 ASDDFEGTYEWEHMSDVAAYFGLDIENSDNKSTLSLQFVDSAADMPLAKMHGAFST 702  
 QY 665 NVVASKELQOQPGSARSTRHLEIELPKEASYQGDHGLGVIPRNYEGIVNRVTRARFGLDASQ 724  
 DB 703 NVVASKELQOQPGSARSTRHLEIELPKEASYQGDHGLGVIPRNYEGIVNRVTRARFGLDASQ 762  
 QY 725 QIRLEAEKEKLAHLPLAKTVSVVEELLQVVELODPVTRTQLRMAAAKTCPPPHKVELEALL 784  
 DB 763 QIRLEAEKEKLAHLPLAKTVSVVEELLQVVELODPVTRTQLRMAAAKTCPPPHKVELEALL 822  
 QY 785 EKOAYKEOVLAKRITMELLEKYPACEMKFSEFIALLPISIRPYYSISSPRVDEKQASI 844  
 DB 823 EKOAYKEOVLAKRITMELLEKYPACEMKFSEFIALLPISIRPYYSISSPRVDEKQASI 882  
 QY 845 TVSVVSGEAWSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIMVGP 904  
 DB 883 TVSVVSGEAWSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIMVGP 942  
 QY 905 TGVAPFRGFVQARKOLKEQOSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAF 964  
 DB 943 TGVAPFRGFVQARKOLKEQOSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAF 1002  
 QY 965 SRMPNQPTYVQHVMEQDGKLIETLDQGAHFYICGDSQMAPAYEATLMKSYADVHOVS 1024  
 DB 1003 SRMPNQPTYVQHVMEQDGKLIETLDQGAHFYICGDSQMAPAYEATLMKSYADVHOVS 1062  
 QY 1025 EADARLWLQLEEKGRYAKDVWAG 1048  
 DB 1063 EADARLWL-QLEEKGRYAKDVWAG 1085  
 RESULT 11  
 AAP81334  
 ID AAP81334 standard; protein; 1144 AA.  
 XX AAP81334;  
 AC AAP81334;  
 XX 19-OCT-1990 (first entry)  
 DT Expression prod. of plasmid pAMP19.  
 DE Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;  
 KW industrial waste.  
 KW JP63044888-A.  
 XX 25-FEB-1988.  
 PD 12-AUG-1986; 86JP-0187713.  
 PF 12-AUG-1986; 86JP-0187713.  
 XX 12-AUG-1986; 86JP-0187713.  
 PR (AGEN ) AGENCY OF IND SCI TECH.  
 PA WPI; 1988-094816/14.  
 XX N-PSDB; AAN81743.  
 DR Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450  
 PT and NADPH-cytochrome p-450 reduction enzyme  
 PS Disclosure; ; p; Japanese.

979	CFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGTVQARKOLKEQOSLGEAHLYFCGRS	938
977	MEVR--KQFRLPFKSTTPVIMVGPGTGIAPFMGFIQERAWLREQKEVGETLLYYGCR	1034
939	PHEDLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKLLIELLQO-GAHF	996
1035	SDELYREELARFHKDGTALQNLVAFSR-EQAHKVVYVOHLLKRDREHLKLIHEGGAHI	1093
997	YTCGDSOMAPAVEATLMKSYADVHVQSEADARLWLOOLEEKGKRYAKDVA	1047
1094	YVCGDARNMAKDVQNTFYDVAEFGPMETQAVDYVKKLMTKGRYSLDWS	1144
RESULT 12		
AAP81337	standard; protein; 1150 AA.	
XX	AAP81337;	
XX	19-OCT-1990 (first entry)	
XX	Expression prod. of plasmid pALP25.	
XX	Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;	
XX	Industrial waste.	
XX	JP63044888-A.	
XX	25-FEB-1988.	
XX	12-AUG-1986; 86JP-0187713.	
XX	12-AUG-1986; 86JP-0187713.	
XX	(AGEN ) AGENCY OF IND SCI TECH.	
XX	WPI; 1988-094816/14.	
XX	N-PSDB; AAN81746.	
XX	Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450	
XX	and NADPH-cytochrome p-450 reduction enzyme	
XX	Disclosure; ; p; Japanese.	
XX	See also AAN81743-85 and AAN81747-48.	
XX	Sequence 1150 AA;	
Query Match	17.7%; Score 968.5; DB 9; Length 1150;	
Best Local Similarity	28.1%; Pred. No. 1.2e-58;	
Matches	320; Conservative 186; Mismatches 468; Indels 163; Gaps 43;	
25	PVQALMKIADELGEIFKEFAPGRVTRYLSSQRLIKEACDESFRDKNLQALKFVDFDAGD	84
63	PHLSLTKLSQQYGDVLIQIRIGSTPVVLSGLNTIKQA-----LVKQGDGPKGR	110
85	GLFTSTHTEKN-----WKKAHNILLPSFSQAMKGY-----HA	117
111	PDLYSFTLIANGQSMTFNPDGSLWAARRL-----AQNALKSFSIASDPTLASSCYLEE	165
118	MMVDIAVOLVQWERLNAD-EHIEVPEDMTRTLTLTGICGFNTFRNFSYRQDPHPITS	176
166	HVSKEAYELISFKQLMAEVGHDFPKYLVSVANVICAICFGRYD--HDDQELLSIVN	223
177	MVRALDEAMNK-----LQANPD---DPAYDENKQFQEDIKVMNDLVDKIIADRKA	225
224	LSNEFGEVTSGYPADFIPIRLYPLNSSLDAPKLNKFEY-----SFMKLIKHEHYR	275
226	SGEQ-----SDDLTHMLNGK-DPETGEPLDENIRYQIITFLIAGHETTSGLLSFALY	278
276	TFEKGHIRIDTSLIEHCQDRLDENANVQLSDDKVVITVDFLFCAGFDITTTAISWSLM	335
279	FLVKNPHVLQKAAEAARVL-VDPVPSYKQVKQKLYGVNVLNEALRLMPTAPAFSL--YA	335
336	YLNTPRIORIKQEEELDTVIGDRDPRLSDRPLYLEAFILETFRHSFVFP-FTIPHS	394
336	KEDTVLGGYPLEKGDMLVLPQLHRKTINGDVEEFRPERFENPS-AIPOHAFKP--	392
395	IRDTSLNGFY-IPKHCYFVQWQVNHQELMGDP-NEFRPERELTSSGTLDKHLSKVI	452
393	FNGQRACIGQOAFALHEATLVGMKHKHDFEDHTNYELDIKET--LTLKP-----EGFV	446
453	LFGLGRKCIGETIGRLEFLFLAILLOQMEFNVSPGKVDWMTPAYGLTLKHARCFQV	512
447	KAKSK-KIPLGIGSPSTEQS-AKKVKAENAHTPLLVLYGSGNMGTAEGTARDLADI	503
513	QMRSSPRAMIOQTAPPVKESFVEKMRKTGRN-----IIVFGSGTGTAEFANRLSKD	567
504	AMSKGPAPOVATLDSH-----AGNLPR--EGAVLIIVTASY-NGHPPDNAAQFVMDQASA	556
568	AHYGRMGASADPEEYDLADLSLPEIDKSLVFCMATYBEGDPTDNAQDFYMLQETDV	627
557	DEVKGVRYSVFGGDKNATWYQKVA---FIDETLAAGAENIADRGEADASDDFGTY.	613
628	D-LTGKFAVFGLGK---TYEHFNAMKYVDQRLQGAQRIEFLGLGDDDDGNLEEDF	682
614	EEMREHWSDAVAFNLDIENSEDNKSLTSLQFVDSADMPKAKH-----	659
683	ITWRFQFPAVCEFFGVEATGEESIRQYELVHE---DMDVAKYITGEMGLKSYENQK	739
660	-----GAFSTNVASKELOQPGSARSTRHLEL-PKEASVQEGDHLGVIPRVNIGTVN	712
740	PPDAKNPFLAATANKLNQ-GTERHLMHLELSDSKIRYESGDHVAVPANDSALYN	798
713	RVTARG--LDASQQLRLBAEELAHPLAKTVSVEELQYVLEQDPVTRTQLRAMAAK	770
799	QIGELGADLDVIMSLNLDSESKKPPCPCTVTRTALTYYVLTITNP-PRTNVLYELAQ	857
771	TVCPP-----HKVEALLEKQAEQVLAARLMLLELKYPAECMKFSEFTALPLSI	824
858	YASESEQEHLHMASSSGEGELYSWVVEARRHILAILQDYPSPRPPIIDLCELLPRL	917
825	RPRTYSSSPRYDEKQASITVSVSGEAWSGYGEYKGIASNYL-AELQEGDT-----IT	878
918	QARYSIASSSSKVPNSVHICAVVEYEAENKSRVN-KGVATSWLRAKEPAGENGRLVLP	976

Db 336 YLVNPRIOKIQEELDTVIGRDRPRLSDRPQLPYLEAFITETFRHSSFPV-FITPHST 394  
QY 336 KEDTVLGGVEPLEKDELAVLPQLHRDRTICWDVEEPRPERFENPS-AIPQHAQK-- 392  
Db 395 IRDTSUNGFY-IPKHCVFVQVQVNDHDELWGP-NEFRPERFLTSSGTLDKHLSEKVI 452  
QY 393 -FGNQRACIGQOQFALHEATLVGLMMLKHDFEDHTNYELDIKET--LTLKP---EGFVV 446  
Db 453 LFGGLKRCICIGETIGRLEVFLEFLAILLQOOMEENVSPGKVDMPAYGLTLKHARCEHFQV 512  
QY 447 KAKSK-----KIPLGIPSPSTEQS-AKVRKAENAHNTPLLVLYGSMNGTAEGTA 497  
Db 513 QMRSSGPRAAAARMIQTAPPVKESSEFVKMKTKGRN-----IIVFYGSQTGAEEFA 567  
QY 498 RDLADIAMSKGPAQOVATLDH-----AGNLPR--EGAVLIVTASY-NGHPPDNKQFVDM 550  
Db 568 NLSKDAHRYGMRGMSADPEEDLADLSLPEIDKSLVFCMATYEGEDPTNAQDFYDM 627  
QY 551 LQASADEVKGVYSVFGCGDKNNWATYQKVP-----FIDETLAAGAENIADRGADAD 607  
Db 628 LQETDVD-LTGKFAVFLGNK-----TYEHENAMGKYVDQRLQEQAGRIEFLGGLDDG 682  
QY 608 DFEQTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQVDSAADPLAKMH----- 659  
Db 683 NLEEDFITWREQFWPACVCEFFGVEATGEESIRQVELVYHE---DMVAKVYTGEMGRK 739  
QY 660 -----GAFSTNVASKELQOQPGSARSTRHLEIEL-PKEASYOEGDHLGVIPRN 706  
Db 740 SYENQKPPDAKNPFLAAVTANRKLNQ-GTERHLMHLELSDSKIRYESGDHVAVYPAN 798  
QY 707 YEGIVNRVTFRG--LDASQQIRLEAEAEKLAHLPLAKTVSVEELLYQVELQDPVTRTOL 764  
Db 799 DSALVNOIGEILLGADLDVMSLNLDESNKKHPCCPTTYRTALTYYLDTNP-PRTNV 857  
QY 765 RAMAAKTVCPP-----HKVLEALLEKQAYKEQVLAKRLTMLELLEKTPACEMKSEFI 818  
Db 858 LYELAQYASEPSEQEDLHKMASSEGKELYLSWVEARRHILAILQDYPSPRPIDHLC 917  
QY 819 ALLPSIRPRYSSTSSPRYDERQASITVSVSGEAWSGEYKGIASNYL-AELQGD- 876  
Db 918 ELLPRLQARYSIASSKVPNSVHCAYAVEYEAKSGRVN-KGATSWLRKAKEPAGENG 976  
QY 877 ----TICFISTQSEFTLPKDPETPLIMVGPOTGVAPFRGVOARKQLKEQOSLGEAHL 932  
Db 977 GRALVPMFVR--KSQRLPFKSTTVIMVGPCTGIAPFMGFTQERAWLREQQKEVGETLL 1034  
QY 933 YFGCRSPHEDLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVOHVMQDGKKLIELLD 991  
Db 1035 YFGCRSDEEDLYREELARFHKDQALQNLNVAFSR-EQAHKYVYQHLKRDREHLKMLTH 1093  
QY 992 Q-GAHFYICGDSQMAPAVEATLMKSYADVHOVSEADARLWLOOLEEGRYAKDYWA 1047  
Db 1094 EGAHYIVCGDARNMAKVONTFYDIVAEFGPMERTQAVDYVKLMTKGRYSLDWS 1150

## RESULT 13

AAP81335

ID AAP81335 standard; protein; 1150 AA.

XX AAP81335;

AC AAP81335;

XX

DT 19-OCT-1990 (first entry)

DE Expression prod. of plasmid pALP1.

XX

DE Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;

XX industrial waste.

KW

XX JP63044888-A;

PN

XX 25-FEB-1988.

PD

XX

PF 12-AUG-1986; 86JP-0187713.  
XX  
PR 12-AUG-1986; 86JP-0187713.  
XX  
PA (AGEN ) AGENCY OF IND SCI TECH.  
XX  
DR WPI; 1988-094816/14.  
DR N-PSDB; AAN81744.  
XX  
PT China fusion enzyme gene - coding oxidation enzyme of cytochrome p-450  
and NADPH-cytochrome p-450 reduction enzyme  
XX  
PS Disclosure; ; p; Japanese.  
XX  
CC See also AAN81743 and AAN81745-48.  
XX  
SQ Sequence 1150 AA;

Query Match 17.6%; Score 962.5; DB 9; Length 1150;  
Best Local Similarity 28.1%; Pred. No. 3.2e-58;  
Matches 319; Conservative 186; Mismatches 469; Indels 163; Gaps 43;

QY 25 PQVALMKTADELGEIFKFEAPORVTRYLSSQRLIKEACDESFRDKNLSOALKFVRDFAGD 84  
Db 63 PHLSTKLSSQQYGDVLIQIRIGSTPVVLSGLNTIKQA-----LVKQGDGDFKGR 110  
QY 85 GLFTSWTEKN-----WKAHNILLPSFSQOAMKY-----HA 117  
Db 111 PLYSFTLIANGQSMFNPDSGLPWAARRL-----AQNALKSFSIASDPTLASSCYLEE 165  
QY 118 MMVDIAVOLVOKWERLNAD-EHIEVPEDMTRTLDTIGLCGFNYRFSFYRDOHPFFITS 176  
Db 166 HVSKEAEYLSIKFQKMAEVGHFDPFKYLVSVANVCAICFRGYD--HDDQELLNIVN 223  
QY 177 MYRALDEAMNK-----LQANPD---DPAYDENKQFQEDIKVMDLVDKIIADKRA 225  
Db 224 LSNEFGVTGSGYPADFIPLRYLPSNLSLDAFKDLNKKFY-----SFMKKLKEHYR 275  
QY 226 SEQ-----SDDLTHMLNGK-DPETGELPDENIRYQIITFLIAGHETTSGLLSFALY 278  
Db 276 TFEKHGIRDITSLIEHCQDRLDENANVOLSDDKVITIVDFGAGDPTITATLSWSLM 335  
QY 279 FLVKNPHVLQAAEEARVL-VDPVPSYQVKQKLYGVKVLNEALRLMPTAPAFSL--YA 335  
Db 336 YLVNPRIOKIQEELDTVIGRDRPRLSDRPQLPYLEAFITETFRHSSFPV-FITPHST 394  
QY 336 KEDTVLGGVEPLEKDELAVLPQLHRDRTICWDVEEPRPERFENPS-AIPQHAQK-- 392  
Db 395 IRDTSUNGFY-IPKHCVFVQVQVNDHDELWGP-NEFRPERFLTSSGTLDKHLSEKVI 452  
QY 393 -FGNQRACIGQOQFALHEATLVGLMMLKHDFEDHTNYELDIKET--LTLKP---EGFVV 446  
Db 453 LFGGLKRCICIGETIGRLEVFLEFLAILLQOOMEENVSPGKVDMPAYGLTLKHARCEHFQV 512  
QY 447 KAKSK-----KIPLGIPSPSTEQS-AKVRKAENAHNTPLLVLYGSMNGTAEGTA 497  
Db 513 QMRSSGPRAAAARMIQTAPPVKESSEFVKMKTKGRN-----IIVFYGSQTGAEEFA 567  
QY 498 RDLADIAMSKGPAQOVATLDH-----AGNLPR--EGAVLIVTASY-NGHPPDNKQFVDM 550  
Db 568 NLSKDAHRYGMRGMSADPEEDLADLSLPEIDKSLVFCMATYEGEDPTNAQDFYDM 627  
QY 551 LQASADEVKGVYSVFGCGDKNNWATYQKVP-----FIDETLAAGAENIADRGADAD 607  
Db 628 LQETDVD-LTGKFAVFLGNK-----TYEHENAMGKYVDQRLQEQAGRIEFLGGLDDG 682  
QY 608 DFEQTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQVDSAADPLAKMH----- 659  
Db 683 NLEEDFITWREQFWPACVCEFFGVEATGEESIRQVELVYHE---DMVAKVYTGEMGRK 739  
QY 660 -----GAFSTNVASKELQOQPGSARSTRHLEIEL-PKEASYOEGDHLGVIPRN 706  
Db 740 SYENQKPPDAKNPFLAAVTANRKLNQ-GTERHLMHLELSDSKIRYESGDHVAVYPAN 798





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RESULT 15
AAP81338
ID AAP81338 standard; protein; 1132 AA.
AC AAP81338;
XX
DT 19-OCT-1990 (first entry)
DE Expression prod. of plasmid pALP4.
DE
KW Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;
KW industrial waste.
XX
PN JP63044888-A.
XX
PD 25-FEB-1988.
XX
PF 12-AUG-1986; 86JP-0187713.
XX
PR 12-AUG-1986; 86JP-0187713.
XX
PA (AGEN ) AGENCY OF IND SCI TECH.
XX
DR WPI; 1988-094816/14.
DR N-PSDB; AAN81747.
XX

Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450
and NADPH-cytochrome p-450 reduction enzyme
PS Disclosure; ; Japanese.
XX
CC See also AAN81743-86and AAN81748.
XX
SQ Sequence 1132 AA;

Query Match 16.6%; Score 906.5; DB 9; Length 1132;
Best Local Similarity 27.2%; Pred. No. 2.6e-54;
Matches 308; Conservative 187; Mismatches 464; Indels 175; Gaps 44;

QY 25 PQVALKMIADLGEIFKFEAPGRVTRYLSSQRLIKEACDESRFDNLSQALKFVRDQAGD 84
DB 63 PHLSLTKLSQYGDVLIQIRIGTPVVLVSLGTLTIKA-----LVKQGDFFKR 110

QY 85 GLFTSWTHKNN-----WKKAHNIILLPSFSQAMKGY-----HA 117
DB 111 POLYSFTLIANGQSMFTFNPDSGLPAAARRL-----AQNALKSFSTASDPTLASSCYLEE 165

QY 118 MVDIAVOIVQKWERLNAD-EHIEVPEDMTLTLDTIGLGFNYRFSNRYRDOQPHFFTS 176
DB 166 HYSKEAYLISAFQKLMAEVGHDPFKYLVSVANVICAICFGRYD--HDDQELLSIVN 223

QY 177 MYRALDEAMNK-----LQANPD---DPAYDENKROFQEDIKVMNDLVDKIIADKA 225
DB 224 LSNEFGEVTCGYPADFPILRYLPNSLDAFKDLNKKFY-----SFMKLLKEHYR 275

QY 226 SGEQ-----SDDLTHMLNGK-DPETGELPDENIRYOIITFLIAGHETTSGLLSFALY 278
DB 276 TFEKGHIRDITSLIEHCODRRLDENANVQLSDDKVTITVFDLFGAGFTDITTAISWSLM 335

QY 279 ELVKNPVHLQAAEEAARVL-VDPVPSYQVQKLVGVNVLNEALRLWETAFAFL--YA 335
DB 336 YLVTPNRIQRIQTELDVTIGRDRPRLSDRQPLYLEAFILETFRHSFVP-FTIPHST 394

QY 336 KEDTVLGPEYPLEKDELMLVLPQLHRDKTIWGDVDEFRPRERFENPS-AIPOHAFKP-- 392
DB 395 IRDTSLNGFY-IPKGCHEVFNQVQVNHQDELNGDP-NEERPERFLTSSGLTDKHLSEKQM 452

QY 393 ----FNGQRACIGQOQFALHEATVLGMMLKHFDEHNTYELDIKETTLLKPEGFVV--- 446
DB 453 EFNVSPEKRV-----DMTPAYGLTLKHARCE----HFQVQMRSS---GPRAAAADRA 497

QY 447 ----KAKSKKIPLGIGIPSPTEQS-AKKVRKKAENAHNTPLLVLYGSMKGTAEGTARDL 500

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Db 498 AAADRAAAADRAMIQTAPPVKESSEFVEKMKTKGRN-----IVFVGSQTAEFPANRL 552
QY 501 ADIAMSKEGFAPOVATLDH-----AGNLPR--EGAVLIVTASY-NGHPPDNKAFQVDMLDQ 553
Db 553 SKDAHRYGIRGMSADPEYDLADLSLPEIDSLVVFVCMATYEGEGPTDNOAQDFYDLQOE 612
QY 554 ASADEVKGVYRVSVFGCGKKNWATTYQKQVPA---FIDETLAARKAGANIADRGADASDDPE 610
Db 613 TDVD-LTGVKFAVFGNGK-----TYEHFNAMKMYVDQRLQLEGAQRIFFELGLGDDGNLE 667
QY 611 GYIEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAAADPLAKMH-----559
Db 668 EDFITWQFNPVAVCEFFGVEATGEESIRQELVYVHE---DMDAKVYVTGEMGRKLSYE 724
QY 660 -----GAFSTNVASKELQOQGSARSTRHLETEL--PKEASYQEGDHLGVIPRNYEG 709
Db 725 NOKPPFDKPNPFLAAVTANRKLNQ-GTERHLMHLELDISDSKIRSESGDHVAVYPANDSA 783
QY 710 IVNRVTARFG--LDASQQIRLEABEKEKLAHLPLAKTVSVVEELQVLEODPVTRTQLRAM 767
Db 784 LVNQIGETILGADLDVIMSLNLDSESNKKHPFPCTTYRTALTYYLDITNP-PRTNVLYE 842
QY 768 AAKTVCCP-----HKVELEALLEKQAYKEQVLAKRLTLMLELEKYPACEMKESFIAL 821
Db 843 LAQYASEPSEQEHLHKMASSSGEGKELYLSWYVEARRHILAILQDYPSLRPPIDHLCCELL 902
QY 822 PSIRPRYISISSPRVDEKQASITVSVSGEAWSGYGEYKGIASNYL-AELQEGDT----876
Db 903 PRLOARYISIASSSKVVHNSVHICAVAVEYEAKSGRVN-KGVATSWLRAKEPAGENGGRA 961
QY 877 -ITCFISTPQSEFTLPKDPETPLIMVGPOTGVAPFRGFVQARKOLKEQSGSLGEAHLXYG 935
Db 962 LVPMEVR--KSQFLPFPKSTTPVIMVGPOTGIAPFMGFIQERAWLREQGKEVGETLLYYG 1019
QY 936 CRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDCKKLIELDQ-G 993
Db 1020 CRSEDELYREELARFHKDQALQTLNVAFSR-EQAHKYVYVQHLKRDREHLKLIHEGG 1078
QY 994 AHFYICGDSQMAPAVEATLMKSYADVHOVSEADARLWLOOLEEKGRYAKDYWA 1047
Db 1079 AHIIYVCGDARNMAKDVQNTFYDVAEFGPMEHTQAVDYVKKLMTKGRYSLDWS 1132

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Search completed: May 29, 2003, 08:28:33  
Job time : 82 secs

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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:22:12 ; Search time 18 seconds  
(without alignments)  
1713.068 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 5457

Sequence: 1 TIKEMPOKTFGELKNLPL.....RLWLOLEKGRYAKDVWAG 1048

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/6C\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	705.5	12.9	588	4	US-09-627-216A-14
2	678	12.4	1429	1	US-07-642-002-2
3	678	12.4	1429	2	US-08-365-486A-13
4	678	12.4	1429	2	US-08-319-866-11
5	678	12.4	1429	4	US-08-880-342-13
6	678	12.4	1430	2	US-08-705-625-4
7	678	12.4	1430	3	US-09-010-998-5
8	678	12.4	1430	4	US-09-220-574-4
9	675	12.4	1433	2	US-08-365-486A-21
10	675	12.4	1433	4	US-09-123-708-4
11	675	12.4	1433	4	US-09-123-624-3
12	675	12.4	1433	4	US-08-880-342-21
13	675	12.4	1434	2	US-08-365-486A-19
14	675	12.4	1434	4	US-08-880-342-19
15	675	12.4	1554	2	US-08-705-625-3
16	675	12.4	1554	3	US-09-010-998-6
17	675	12.4	1554	4	US-09-220-574-3
18	665.5	12.2	1144	2	US-08-147-812-5
19	665.5	12.2	1144	2	US-08-319-866-12
20	664.5	12.2	1144	4	US-09-123-708-2
21	664.5	12.2	1144	4	US-09-123-624-2
22	662	12.1	1146	4	US-09-126-109-12
23	654.5	12.0	693	1	US-08-553-279-2
24	650	11.9	1153	1	US-08-314-917-2
25	650	11.9	1153	1	US-08-265-046-2
26	650	11.9	1153	2	US-08-465-522-2
27	650	11.9	1153	5	PCT-US93-11401-2

28	650	11.9	1153	5	PCT-US95-07849-2	Sequence 2, Appli
29	599.5	11.0	1205	2	US-08-319-866-10	Sequence 10, Appl
30	599.5	11.0	1205	4	US-09-123-708-6	Sequence 6, Appli
31	599.5	11.0	1205	4	US-09-123-624-6	Sequence 6, Appli
32	598.5	11.0	1205	1	US-07-908-245-2	Sequence 2, Appli
33	597	10.9	679	4	US-09-302-620B-83	Sequence 83, Appl
34	593	10.9	679	4	US-09-302-620B-84	Sequence 84, Appl
35	583.5	10.7	629	4	US-09-134-001C-4394	Sequence 4394, Ap
36	564.5	10.3	1350	2	US-08-319-866-9	Sequence 9, Appli
37	460	8.4	576	3	US-08-948-564-16	Sequence 16, Appl
38	391.5	7.2	540	4	US-09-302-620B-98	Sequence 98, Appl
39	383.5	7.0	540	4	US-09-302-620B-99	Sequence 99, Appl
40	378.5	6.9	504	1	US-08-457-274A-25	Sequence 25, Appl
41	378.5	6.9	504	5	PCT-US95-05758-25	Sequence 25, Appl
42	370.5	6.8	503	4	US-09-144-367-2	Sequence 2, Appli
43	352	6.5	522	4	US-09-302-620B-97	Sequence 97, Appl
44	349	6.4	512	4	US-09-302-620B-102	Sequence 102, App
45	349	6.4	522	4	US-09-302-620B-96	Sequence 96, Appl

ALIGNMENTS

RESULT 1

US-09-627-216A-14  
; Sequence 14, Application US/09627216A  
; Patent No. 6368837  
; GENERAL INFORMATION:  
; APPLICANT: Sariasiani, Sima F  
; APPLICANT: Tang, Xiao-Song  
; APPLICANT: Qi, Wei Wei  
; APPLICANT: Vannelli, Todd  
; APPLICANT: Gatenby, Anthony  
; TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid  
; FILE REFERENCE: BCI009 US NA  
; CURRENT APPLICATION NUMBER: US/09/627,216A  
; CURRENT FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 60/147,719  
; PRIOR FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 14  
; LENGTH: 588  
; TYPE: PRT  
; ORGANISM: Helianthus tuberosus  
US-09-627-216A-14

Query Match		12.98;	Score 705.5;	DB 4;	Length 588;
Best Local Similarity		31.98;	Pred. No. 2.1e-53;		
Matches 189;		Conservative 92;	Mismatches 245;	Indels 67;	Gaps 19;
QY	499	DLADIAMKGFAPQVATLDSHAGNLPREGAVLIVTASY-NHPPDPNAKQFVDWLDOASAD	557		
Db	18	DLDYYA-----ADDEYAEKFKETFAFFFLATYGDGPTDNNARYKWTGEG---	65		
QY	558	EYKGV-----RYSVFGCGDKNWTYQKVPAFIDETLAAKGAENIADGEADSDDEFT	612		
Db	66	DDRGVWLEKLYHGVFGLGNKQY-EHFNKIALVWDEGLTEQGAQKRFVPGVGLDDQSD	124		
QY	613	YEWREHMSDVAAYNFLDIENSEDNKS-----TSL-----QFVDSAADMPL	655		
Db	125	FSAWKELWPELDQLL-LD-----EDDKTAATPYTAIPEYRVFVHDKPDTFSENHSOTNG	179		
QY	656	AKMHA-----FSTNVASKELQPGQSARSTRHLELPKEA-SYQEGHGLGVIPRNYEGIV	711		
Db	180	HTVHDQHPCRSNVAVKKELHTPESDRSCHLEFDISHTGLSVETGHHGVYCNLEVV	239		
QY	712	NRVTRFGLDASQOIRLEAEKEEKLHL-----PLAKTVSVEELQYVELQDPVTRTQL	764		
Db	240	EEAEKLIGLPADTYFSLHIDNEDGTPLGGFTLQPPPPCTLRKALTNYADLLSSPKSTL	299		
QY	765	RAMAAKTVCPHPKVELEALLE---KQAYKEQVLAKRUTMLELLEKYPACEMKESEFT-AL	820		

Db 300 LALAAHASDATEADRIQLFASREGKDEYAEWIVANQORSLEVEAPPSAKPIGVFFAAI 359  
QY 821 LPSIRPRYSISSPRVDEKQASITVSVSGAWSGYGYKGIASNY-----LAEORG 874  
Db 360 APRLQPRYSISSPKWPNRHVTCALVY-EKTPGRIHKGICSTWMMNAVPLTENQDC 418  
QY 875 DTITCFISTPQSEFTLPKDPETPLIMVPGTGVAPFQVQARKQLKEQOQSLGEAHLFY 934  
Db 419 SSAPFVRT--SNFRLPADPKVPVIMIGPGTGLAPRGLQERLALKESGTELQOSILFF 476  
QY 935 GCRSPHEDLYQBELENAQSEGIIT-LHTAFSRMPNPKTYVQHVQMEQDKKLIELLDG 993  
Db 477 GCRNRKVDYFENELNMFENGALSSELDMAFSR-EGASKEYVQHKMSQKASDIWNMLSEG 535  
QY 994 AHFYICGDSQMAPAVEATLMKSYADVHOVSADARLWLOQLEEKRYAKDVW 1046  
Db 536 AYLVCGDAGKMAKDVHRLHTIVQEQNLDSKAEIYVKNLQMSGRYLRDVW 588  
  
RESULT 2  
US-07-642-002-2  
; Sequence 2, Application US/07642002  
; Patent No. 5268465  
; GENERAL INFORMATION:  
; APPLICANT: Bredt, David S.  
; APPLICANT: Hwang, Paul M.  
; APPLICANT: Reed, Randall  
; APPLICANT: Snyder, Solomon H.  
; TITLE OF INVENTION: Purification and Molecular Cloning of Nitric  
; TITLE OF INVENTION: Oxide Synthase  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner, Birch, McKie & Beckett  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/642,002  
; FILING DATE: 19910118  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 1107.033576  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 296-5500  
; TELEFAX: (202) 296-7830  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1429 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-642-002-2  
  
Query Match 12.4%; Score 678; DB 1; Length 1429;  
Best Local Similarity 28.2%; Pred. No. 2.6e-50;  
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;  
  
QY 457 GIPSPSTQSAKVRKAE-----NAHTPTLLVYGSNMGTAEGTARDIADIA 504  
Db 718 GTNGPTTKRATGFRKLAEAVEKFSAKLMQAMKVRKATILYATETGKSQAYAKTICEIF 777  
QY 505 MSKGAPAPVATDSDHAGNLPRGAVLIVTASY-NGHPDPNNAKOF----- 547  
Db 778 KHAFDAKMSMEYDIIVHLEALVIVTSTGTGNDPPENGKFGCALMEMRHPNSVQEE 837

QY 548 -----VDWLQD--ASADEVKGVYSVFCGCGDKNNWATTYQKVP 582  
Db 838 RKSJKVRFNSVSSYSDSRKSSGDPDLRDNFESTGPLANRFSVFGLSR-----AYPHFC 893  
QY 583 AF---IDETLAAGAENIADRGADASDDFEGTYEEWRHMHMSDVAAYFNL--DIENSED 637  
Db 894 AFGHAVDTLLEELGGERILKMRGDBLCQGEAEFRTWAKKFKAAKADVFCVGDVNIIEP 953  
QY 638 NKSTLS-----LQFVDSADMP--LAKMH--GAFSTNVVASKELQPGSGARSIR 682  
Db 954 NNSLISNDRSWKRNKFRITYVAEPDLTQGLSNVHKRVSAARLLSRQLQSPKFSRSTI 1013  
QY 683 HLEIEL--PKEASYEGDHLGVIIPRYEGIVNRVTARF--GLDASQOIRLEAEEELLAHL 738  
Db 1014 FYRLHTNGQELQYQXQGDHLGVFPNGHEDLVNALIERLEDAPPANHVVKVMELEENTAL 1073  
QY 739 PIAKTVSVEELL-----QYVELQDPVTRTQLRAMAATVCPPHKVELEALLE-KQ 787  
Db 1074 GVISNWKDESRLPPCTIFQAFKYILDITTPPTPLQIQPASPATNEKEKORLLVLSKGLQ 1133  
QY 788 AYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLSIRPRYSISSPRVDEKQASITVS 847  
Db 1134 EYEEWKGKNTMVEVLEEFPSIQMPATLLLTQLSLQPRYSISSPPDMPDEVHLTVA 1193  
QY 848 VVSGEAWSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVPGTG 906  
Db 1194 IVSYHTRDGEVPHHGVCSWLNRIQADDDVPCFVRGAPS-FHLPNPNQVPCILVPGTG 1252  
QY 907 VAPFPGFVQARK-QLKEQOQSLGEAHLFYGCRSPHEDLYQBELENAQSEGII-TLHTAF 964  
Db 1253 IAPFRSFQOQRFDIQHKGMNCPMVLVFCGRQSKIDHIYREETLQAKNKGVFRELYTAY 1312  
QY 965 SRMPNPKTYVQHVQMEQDKKLI--ELLQGAHFYICGDSQMAPAVEATLMKSYADVHQ 1022  
Db 1313 SREPRPKYVQDVVLQEQLAESVYRALKEQGGHIVCGDVTMAADVLA-IGRIMTQOQK 1371  
QY 1023 VSEADARLWLOQLEEKRYAKDVW 1046  
Db 1372 LSEEDAGVFSRLRDNRYHEDIF.1395  
  
RESULT 3  
US-08-365-486A-13  
; Sequence 13, Application US/08365486A  
; Patent No. 5834306  
; GENERAL INFORMATION:  
; APPLICANT: Webster, Keith A.  
; APPLICANT: Bishopric, Nanette H.  
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
; TITLE OF INVENTION: Therapeutic Constructs  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/365,486A  
; FILING DATE: 23-DEC-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 8255-0018  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1429 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-365-486A-13

Query Match 12.4%; Score 678; DB 2; Length 1429;  
Best Local Similarity 28.2%; Pred. No. 2.6e-50;  
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;

QY 457 GIPSPTEQSAKKVRKAE-----NAHNTPLLVLYGSGMGTAGTARDLADIA 504  
DB 718 GTNGTTPKRAIGFKLAFAVKSALMGQAMAKRVKATILYATETGKSOAYAKTICEIF 777  
QY 505 MSKGFAPQATLDSHAGNLPREGAVLIVTASY-NHPPDNAKQF----- 547  
DB 778 KHAFDAKAMSEYDIVHLEHEALVLVVTSTFCNGDPPENGKEFGCALMEMRHPNSVQEE 837  
QY 548 -----VDWLQD-ASADEVKGVRYSVFGCGDKNWAATYQKVP 582  
DB 838 RKSQKVRNFSVSSYSRKSNGDGLRDNFSTGTPLANRVFVGLGSR-----AYPHFC 893  
QY 583 AF---IDETLAAGAENIADRGADASDDFEGTYEWEHMSDVAAYFNL--DIENSED 637  
DB 894 AFGHAVDTLLEELGGERILKMRGDELCOGEAFRTWAKVFKAACDVFCVGDVNIERP 953  
QY 638 NKSTLS-----LOFVDSAADMP--LAKMH--GAFSTNVVASKELQOPGSARSTR 682  
DB 954 NNSLISNDRSWKRNKFLTYVAEAPDLTQGLSNVHKRVSAARLLSQNLQSPKFSRSTI 1013  
QY 683 HLEIEL--PKEASYQEGDHLGVIPRNYEGIVNVRTARF--GLDASQOIRLEAEKEHLAHL 738  
DB 1014 FVRLHTNGNQLQYQPGDHLGVFPNGHEDLVNALIERLEDAPPANHVVKVEMLEERTAL 1073  
QY 739 PLAKTVSVEELL-----QYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE-KQ 787  
DB 1074 GVISNWKDESRLPCTIFQAFKYLDITPTPLQLOQFASLATNEKEKORLLVLSKGLQ 1133  
QY 788 AYKEQVLAKRLTMLELLEKYPACEMKFSFIALPSPRIYSSISPRVDEKQASITVS 847  
DB 1134 EYEWKGNKPTMVEVELEFPSPQMPATLLLTQLSLQPRYSSISPPDMYPDEVHUTVA 1193  
QY 848 VSGEAWSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLMVGPCTG 906  
DB 1194 IVSYTRDGGPVHGGVCSWLNRIQADVVPCFVRGAPS-FHLPRNPQVPCILVGPCTG 1252  
QY 907 VAPFRGFQARK-QLAKEQGSGLGEAHLIFGCRSPHEDLYOELENAQSGIITLHTAF 964  
DB 1253 IAFRSEFWOQRFDIHQKMNPCPMVLVFCROSKIDHIYRETLQAKNGKGVRELYTAY 1312  
QY 965 SRMNPQKTYVQVHMSQDGKKLI--ELLDGAHYICGDSQMAPAVEATLMKSYADVHQ 1022  
DB 1313 SREPRKPKYQDVLQELAESYVRALKQEGGHIYVCGDVTMAADVLA-IQRIMTQOGK 1371  
QY 1023 VSEADARLWLQLEEKGRVAKDVW 1046  
DB 1372 LSEEDAGVFISRLRDDNRYHEDIF 1395

RESULT 4

US-08-319-866-11  
Sequence 11, Application US/08319866  
Patent No. 5929223  
GENERAL INFORMATION:  
APPLICANT: Tully, Timothy P.  
APPLICANT: Yiu, Jerry C.  
APPLICANT: Regulski, Michael  
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES  
ASSOCIATED WITH LONG-TERM MEMORY

NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,866  
FILING DATE: 7-OCT-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL94-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1429 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-319-866-11

Query Match 12.4%; Score 678; DB 2; Length 1429;  
Best Local Similarity 28.2%; Pred. No. 2.6e-50;  
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;

QY 457 GIPSPTEQSAKKVRKAE-----NAHNTPLLVLYGSGMGTAGTARDLADIA 504  
DB 718 GTNGTTPKRAIGFKLAFAVKSALMGQAMAKRVKATILYATETGKSOAYAKTICEIF 777  
QY 505 MSKGFAPQATLDSHAGNLPREGAVLIVTASY-NHPPDNAKQF----- 547  
DB 778 KHAFDAKAMSEYDIVHLEHEALVLVVTSTFCNGDPPENGKEFGCALMEMRHPNSVQEE 837  
QY 548 -----VDWLQD-ASADEVKGVRYSVFGCGDKNWAATYQKVP 582  
DB 838 RKSQKVRNFSVSSYSRKSNGDGLRDNFSTGTPLANRVFVGLGSR-----AYPHFC 893  
QY 583 AF---IDETLAAGAENIADRGADASDDFEGTYEWEHMSDVAAYFNL--DIENSED 637  
DB 894 AFGHAVDTLLEELGGERILKMRGDELCOGEAFRTWAKVFKAACDVFCVGDVNIERP 953  
QY 638 NKSTLS-----LOFVDSAADMP--LAKMH--GAFSTNVVASKELQOPGSARSTR 682  
DB 954 NNSLISNDRSWKRNKFLTYVAEAPDLTQGLSNVHKRVSAARLLSQNLQSPKFSRSTI 1013  
QY 683 HLEIEL--PKEASYQEGDHLGVIPRNYEGIVNVRTARF--GLDASQOIRLEAEKEHLAHL 738  
DB 1014 FVRLHTNGNQLQYQPGDHLGVFPNGHEDLVNALIERLEDAPPANHVVKVEMLEERTAL 1073  
QY 739 PLAKTVSVEELL-----QYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE-KQ 787  
DB 1074 GVISNWKDESRLPCTIFQAFKYLDITPTPLQLOQFASLATNEKEKORLLVLSKGLQ 1133  
QY 788 AYKEQVLAKRLTMLELLEKYPACEMKFSFIALPSPRIYSSISPRVDEKQASITVS 847  
DB 1134 EYEWKGNKPTMVEVELEFPSPQMPATLLLTQLSLQPRYSSISPPDMYPDEVHUTVA 1193  
QY 848 VSGEAWSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLMVGPCTG 906

Db 1194 IVSYHTRDGEVPHVHCVCSSWLNRIQADDDVPCFVRGAPS-FHLPNRPQVPCILVGPSTG 1252  
QY 907 VAPFRGCVQARK-OLKEQOSLGEAHLVYGCSPHEDYLYQLELENAQSEGII-TLHTAF 964  
Db 1253 IAPFRSFWOORFDIOHKGMNCPMVLVFGCRQSKIDHIYREETLQAKNKGVRRELYTAY 1312  
QY 965 SRMPNPKTYVQHVMEQDGKKLI--ELLDQGAHFYICGDSQMAPAVEATLMKSYADVHQ 1022  
Db 1313 SREPDPRKYYQDVVLQELQALAESVYRALKEGGHIVCGDVTMAADVLKA-IQRIWTOQOK 1371  
QY 1023 VSEADARLWLOOLEKGRYAKDVW 1046  
Db 1372 LSEEDAGVFISRLDDNRYHEDIF 1395

## RESULT 5

US-08-880-342-13  
; Sequence 13, Application US/08880342  
; Patent No. 6218179  
; GENERAL INFORMATION:  
; APPLICANT: Webster, Keith A.  
; APPLICANT: Bishopric, Nanette H.  
; APPLICANT: Murphy, Brian  
; APPLICANT: Laderoute, Keith R.  
; APPLICANT: Green, Christopher J.  
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
; TITLE OF INVENTION: Therapeutic Constructs  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/880,342  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/IB95/00996  
; FILING DATE: 13-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/365,486  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 8255-0018.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1429 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-880-342-13

Query Match 12.4%; Score 678; DB 4; Length 1429;  
Best Local Similarity 28.2%; Pred. No. 2.6e-50;  
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;  
QY 457 GIPSPSTEQSAKKVRKAE-----NAHNTPLLVLYGSNNGTAEGTARDIADIA 504  
Db 718 GTNGTPTKRAITGFRKLAEVKFSAKLMQAMAKRVKATILYATETGSKSQAAYKTLCIEIF 777

QY 505 MSKGFAPOAVTLD SHAGNLPRREGAVLIVTASY-NGHPPDNKOF----- 547  
Db 778 KHAFDAKMSMEYDIIVLHEALVIVTSTFGNGDPPENGKFCGALMEMRHPNSVQEE 837  
QY 548 -----VDWLQD-ASADEVKGVRYSVFSGCDKNWATTYQKYP 582  
Db 838 RKSXYKRVNSVSSDSRKSXGDPDLRDNFESTGPLANVRFVSFGLGSR-----AYPHFC 893  
QY 583 AF---IDETLAAGAENIADRGEADSDDFEGTYEWEHRHMSDVAAYFNL--DIENSED 637  
Db 894 AFGHAVDTLLEELGGERILKMRGDELQGEAFRTWAKKVFKAACDVCVGDVNVIEKP 953  
QY 638 NKSTLS-----LQFVDSAADMP--LAKMH--GAFSTNVYVASKELQOPGSGARSTR 682  
Db 954 NNSLISNDRSWRNKFRITYVAEPDLTQGLSNVHKRVSAARLLSRNLQSPKFSRSTI 1013  
QY 683 HLEIEL--PKEASYQEGDHLGVIPIRNYEGIVNRVTRF--GLDASQOIRLEAEEKLAHL 738  
Db 1014 FVRLHTNGNOELQYQGDHLGVFPGNHEDLVNALTIERLEDAPPANHVVKVMELEERTAL 1073  
QY 739 PLAKTVSVEELL-----QYVELODPVTRTOLRAMAAKTVCPPHKVELEALLE-KQ 787  
Db 1074 GVISNWKDESRLPCTIFQAFKYLDITPTTPLLQOQFASLATNEKEKORLLVLSKGLQ 1133  
QY 788 AYKEQVLAKRLTMLELLEKYPACEMKFSFIALLPSIRPRYYSISSPRVDEKQASITVS 847  
Db 1134 EYEENKWKGNPTMVEVLEFPISQMPATLLLTQLSLQPRYYSISSPDYMDVHLTVA 1193  
QY 848 VVSGEAWSGYGE-YKGIASNYLAELQEGDTTCFTSTPQSEFTLPKDPPTPLIMVGPSTG 906  
Db 1194 IVSYHTRDGEVPHVHCVCSSWLNRIQADDDVPCFVRGAPS-FHLPNRPQVPCILVGPSTG 1252  
QY 907 VAPFRGCVQARK-OLKEQOSLGEAHLVYGCSPHEDYLYQLELENAQSEGII-TLHTAF 964  
Db 1253 IAPFRSFWOORFDIOHKGMNCPMVLVFGCRQSKIDHIYREETLQAKNKGVRRELYTAY 1312  
QY 965 SRMPNPKTYVQHVMEQDGKKLI--ELLDQGAHFYICGDSQMAPAVEATLMKSYADVHQ 1022  
Db 1313 SREPDPRKYYQDVVLQELQALAESVYRALKEGGHIVCGDVTMAADVLKA-IQRIWTOQOK 1371  
QY 1023 VSEADARLWLOOLEKGRYAKDVW 1046  
Db 1372 LSEEDAGVFISRLDDNRYHEDIF 1395

## RESULT 6

US-08-705-625-4  
; Sequence 4, Application US/08705625  
; Patent No. 5908756  
; GENERAL INFORMATION:  
; APPLICANT: Snyder, Solomon H.  
; APPLICANT: Jaffrey, Samie R.  
; TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric  
; TITLE OF INVENTION: Oxide Synthase  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff  
; STREET: 1001 G Street, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001-4597  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/705,625  
; FILING DATE: 30-AUG-1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.57071  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1430 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-705-625-4

Query Match 12.4%; Score 678; DB 2; Length 1430;  
Best Local Similarity 28.2%; Pred. No. 2.6e-50;  
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;  
QY 457 GIPSPSTQSAKVRKAE-----NAHNTPLLVYSGNMGTAEGTARDLADIA 504  
DB 718 GTNGTPTKRAIGFKKLAEEVFSKALMGQAMAKRVKATILYATETGKSQAYAKTLCIEIF 777  
QY 505 MSKGFAPQAVATLDSHAGNLPREGAVLIVTASY--NGHPPDNAKQF----- 547  
DB 778 KHAFDKAMSMEEYDIVHLEHEALVIVTSTFTGNGDPPENGKEKFCALMEMRHPNSVQEE 837  
QY 548 -----VDWLDQ--ASADEVKGVRYSVFGCGDKKNWATYQKVP 582  
DB 838 RKSXYKVRNVSYSYSDSKSSGDPDLRDNFESTGPLANVRFVSFVGLGSR----AYPHFC 893  
QY 583 AF----IDETLAAGAENIADRGADSDDFEGTYEEWRHMSDVAAYFNL--DIENSED 637  
DB 894 AFGHAVDTLLEELGERILKMRGDELCCGEEAFTWAKVKVKAACDFVCVGDVNVTEKP 953  
QY 638 NKSTLS-----LQFVDSAADMP--LAKMH--GAFSTNVVASKELQOPGSASTR 682  
DB 954 NNSLISNDRSKRNRKFRITYVAEAPDLTQGLSNVHKRVSAARLLSRQLQSPKFSRSTI 1013  
QY 683 HLEIEL--PKEASVQEGDHLGVIIPRYEGIVNRYTARF--GLDASQOIRLEAEKEKLAHL 738  
DB 1014 FVRLHTNGNQLQYQPGDHLGVFPNGNHDVLNALTIERLEDAPPANHVVKVEMLEERNAL 1073  
QY 739 PLAKTVSVEELL-----QYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE--KQ 787  
DB 1074 GVISNWKDESRLPCTTFQAFKYILDITPTPLQLOQFASLATNEKEKQRLVLSKGLQ 1133  
QY 788 AYKEQVLAKRLTMLELEKYPACEMKPFSEFTALLPSIRPRYSISSSPRVDEKQASITVS 847  
DB 1134 EYEWKGNKNTMVEVLEEFPSIQMPATLLTLQLSLQPRYSISSSPDMPYDEVHLTVA 1193  
QY 848 VVSGEANSGYCE--YKGIASNYLAELOEGDTITCFISTPQSEFTLPKQDPTLIMVPGTG 906  
DB 1194 IVSTHTRDGEVPHVHCSSWLNRLQADDVPCFVRGAPS--FHLPRNPQVCIILVPGTG 1252  
QY 907 VAPFRGFVQARK--OLKEQGQSLGEAHLYFGCRSPHEDLYQEELENAQSEGII--TLHTAF 964  
DB 1253 IAPFRSQWQRFQDIQHKGMNCPMVLVFGCRQSKIDHIYREETLQAKNKGFRLEYTAY 1312  
QY 965 SRMPNQPKTYVQHVMEQDGKKLI--ELLDQGAHYICGDSQMAPAVEATLMKSYADVHQ 1022  
DB 1313 SREDPKPKYQDVLQELQALBSYRALKEQGHYIVCGDVTMAADVLA--IQRTMTQOGK 1371  
QY 1023 VSEADARLWLOOLEEKGRYAKDVW 1046  
DB 1372 LSEEDAGVFISRLKDDNRIYHEDIF 1395

RESULT 7  
US-09-010-998-5  
; Sequence 5, Application US/09010998  
; Patent No. 6103872

GENERAL INFORMATION:  
APPLICANT: Snyder, Solomon  
APPLICANT: Jaffrey, Samie  
APPLICANT: Snowman, Adele  
APPLICANT: Eliasson, Mikael  
APPLICANT: Cohen, No. 6103872m  
TITLE OF INVENTION: CAPON, a protein that binds  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff  
STREET: 1001 G Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/010.998  
FILING DATE: 22-JAN-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A  
REGISTRATION NUMBER: 32141  
REFERENCE/DOCKET NUMBER: 01107.73424  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1430 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6103872e  
US-09-010-998-5

Query Match 12.4%; Score 678; DB 3; Length 1430;  
Best Local Similarity 28.2%; Pred. No. 2.6e-50;  
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;  
QY 457 GIPSPSTQSAKVRKAE-----NAHNTPLLVYSGNMGTAEGTARDLADIA 504  
DB 718 GTNGTPTKRAIGFKKLAEEVFSKALMGQAMAKRVKATILYATETGKSQAYAKTLCIEIF 777  
QY 505 MSKGFAPQAVATLDSHAGNLPREGAVLIVTASY--NGHPPDNAKQF----- 547  
DB 778 KHAFDKAMSMEEYDIVHLEHEALVIVTSTFTGNGDPPENGKEKFCALMEMRHPNSVQEE 837  
QY 548 -----VDWLDQ--ASADEVKGVRYSVFGCGDKKNWATYQKVP 582  
DB 838 RKSXYKVRNVSYSYSDSKSSGDPDLRDNFESTGPLANVRFVSFVGLGSR----AYPHFC 893  
QY 583 AF----IDETLAAGAENIADRGADSDDFEGTYEEWRHMSDVAAYFNL--DIENSED 637  
DB 894 AFGHAVDTLLEELGERILKMRGDELCCGEEAFTWAKVKVKAACDFVCVGDVNVTEKP 953  
QY 638 NKSTLS-----LQFVDSAADMP--LAKMH--GAFSTNVVASKELQOPGSASTR 682  
DB 954 NNSLISNDRSKRNRKFRITYVAEAPDLTQGLSNVHKRVSAARLLSRQLQSPKFSRSTI 1013  
QY 683 HLEIEL--PKEASVQEGDHLGVIIPRYEGIVNRYTARF--GLDASQOIRLEAEKEKLAHL 738  
DB 1014 FVRLHTNGNQLQYQPGDHLGVFPNGNHDVLNALTIERLEDAPPANHVVKVEMLEERNAL 1073

QY 739 PLAKTVSVEELL-----QYVELQDPVTRTOLRAMAAKTVCPHPKVELEALLE-KQ 787  
Db 1074 GVISNWKDESRLPPCTIFQAFKYYLDITPTPTPLQLOQFASLATNEKEKORLIVLSKGLQ 1133  
QY 788 AYKEQVLAKRLTLMLELLEKYPACEMKFSFIALPSIRPRYSISSPRVDEKQASITVS 847  
Db 1134 EYEEKWKGNPTMVELEFPSTQMPATLLLTQLSLQPRYSISSSPDMYPDEVHLTVA 1193  
QY 848 VSGEAWSGYGE-YKGIASNYLAELQEGDITITCFISTPOSEFTLPKDPDPTPLIMVPGTG 906  
Db 1194 IVSYHTRDGEVPHHGVCSWLNRIQADVVPCFVGRGAS-FHLPNRPQVPCILVPGTG 1252  
QY 907 VAPFRGVOARK-OLKEQOQSLGEAHLFYGCSPHEDYLYQEBLENAQSEGII-TLHTAF 964  
Db 1253 IAPFRSFQORQFDIHKGMNCPMVLVFCGRQSKIDHIYRETLQAKNKGVRRELYTAY 1312  
QY 965 SRMPNPKTYVQHVMEQDGKKLI--ELLQOQAHFYICGDSQMAPAVEATLMKSYADVHQ 1022  
Db 1313 SREPDPRKYYQDVQLQELAEYSYRALKEQGGHYYVCGDVTMAADVLKA-IQRIIMTQOGK 1371  
QY 1023 VSEADARLWLOOLEEKGRYAKDVW 1046  
Db 1372 LSEEDAGVFISRLDDNRHEDIF 1395

## RESULT 8

US-09-220-574-4  
; Sequence 4, Application US/09220574  
; Patent No. 6168926  
; GENERAL INFORMATION:  
; APPLICANT: Snyder, Solomon H.  
; APPLICANT: Jaffrey, Samle R.  
; TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric  
; TITLE OF INVENTION: Oxide Synthase  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff  
; STREET: 1001 G Street, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001-4597  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/220,574  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/705,625  
; FILING DATE: 30-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kegan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.57071  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1430 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-09-220-574-4

Query Match 12.4%; Score 678; DB 4; Length 1430;  
Best Local Similarity 28.2%; Pred. No. 2.6e-50;

Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;  
QY 457 GIPSPSTEQSAKKVRKAE-----NAHNTPLLVLYGSGNMGTAEGTARDADIA 504  
Db 718 GNGTPTTKRRATGFKLAEAIVKFAKLMQAMAKRVKATILITATETGKSOAYAKTICEIF 777  
QY 505 MSKGAPOVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKOF----- 547  
Db 778 KHAFDAKAMSMEEYDIVHLEHEALVLVTVTSTFGNGDPENGKFGCALMEMRHPNSVQEE 837  
QY 548 -----VDWLQO-ASADEVKGVYRYSVFCGCKNNAWTTQKVP 582  
Db 838 RKSXYKRFNSVSSYSRKSXSGDGPDLRDNFESTGPLANVRFVSFGLGRS----AYPHFC 893  
QY 583 AF---IDETLAAGAENIADRGADASDDFEGTYEEMREHMSDVAAYNL--DIENSED 637  
Db 894 AGHVAVDTLLELGGRIILKMGREGDELCOGEAFRTWAKKVFKAACDVCVGDVDVNIKP 953  
QY 638 NKSTLS-----LQFVDSADMP--LAKMH--GAFSTNVVASKELQOPGSAARSTR 682  
Db 954 NNSLISNDRSWKRNKFRLTYYAEAPDLTQGLSNVHKRYSAARLLSRQNLQSPKFSRSTI 1013  
QY 683 HLEIEL--PKEASYQEGDHLGVIPRNYEGIVNRVTARF--GLDASQOIRLEAEKEKLAHL 738  
Db 1014 FVRLHTNGQELQYQPGDHLGVFPNGHEDLVNALIERLEDAPPANHVVKVEMLEERTAL 1073  
QY 739 PLAKTVSVEELL-----QYVELQDPVTRTOLRAMAAKTVCPHPKVELEALLE-KQ 787  
Db 1074 GVISNWKDESRLPPCTIFQAFKYYLDITPTPTPLQLOQFASLATNEKEKORLIVLSKGLQ 1133  
QY 788 AYKEQVLAKRLTLMLELLEKYPACEMKFSFIALPSIRPRYSISSPRVDEKQASITVS 847  
Db 1134 EYEEKWKGNPTMVELEFPSTQMPATLLLTQLSLQPRYSISSSPDMYPDEVHLTVA 1193  
QY 848 VSGEAWSGYGE-YKGIASNYLAELQEGDITITCFISTPOSEFTLPKDPDPTPLIMVPGTG 906  
Db 1194 IVSYHTRDGEVPHHGVCSWLNRIQADVVPCFVGRGAS-FHLPNRPQVPCILVPGTG 1252  
QY 907 VAPFRGVOARK-OLKEQOQSLGEAHLFYGCSPHEDYLYQEBLENAQSEGII-TLHTAF 964  
Db 1253 IAPFRSFQORQFDIHKGMNCPMVLVFCGRQSKIDHIYRETLQAKNKGVRRELYTAY 1312  
QY 965 SRMPNPKTYVQHVMEQDGKKLI--ELLQOQAHFYICGDSQMAPAVEATLMKSYADVHQ 1022  
Db 1313 SREPDPRKYYQDVQLQELAEYSYRALKEQGGHYYVCGDVTMAADVLKA-IQRIIMTQOGK 1371  
QY 1023 VSEADARLWLOOLEEKGRYAKDVW 1046  
Db 1372 LSEEDAGVFISRLDDNRHEDIF 1395

## RESULT 9

US-08-365-486A-21  
; Sequence 21, Application US/08365486A  
; Patent No. 5834306  
; GENERAL INFORMATION:  
; APPLICANT: Webster, Keith A.  
; APPLICANT: Bishopric, Nanette H.  
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
; TITLE OF INVENTION: Therapeutic Constructs  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25



; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/365,486A  
 ; FILING DATE: 23-DEC-1994  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sholtz, Charles K.  
 ; REGISTRATION NUMBER: 38,615  
 ; REFERENCE/DOCKET NUMBER: 8255-0018  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 324-0880  
 ; TELEFAX: (415) 324-0960  
 ; INFORMATION FOR SEQ ID NO: 21:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1433 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-365-486A-21

Query Match 12.4%; Score 675; DB 2; Length 1433;  
 Best Local Similarity 28.0%; Pred. No. 4.9e-50;  
 Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

QY	457	GIPSPSTEQSAKKVRKAE-----NAHNTPLLVLYGSMGTAGCTARDLADIA	504
DB	722	GTNGTPTKRAIGFKLAELAEVKSALMGQAMAKRVKATILYATETKSAQYAKTICEI-	780
QY	505	MSKGFAPQVATLDSH-AGNLPREGAVLIVTASY-NGHPPDNAKOF-----	547
DB	781	FKHAFDAKVMSEYDIVLHEHTLVIVTSTFGNGDPPENGKFGCALMEMRHPNSVQE	840
QY	548	-----VDWLQD-ASADEVKGVRYSVFGCGDKNNWATTYQKV	581
DB	841	ERKSYKVRFSVSYSDSKSGDGLDRNDFESAGPLANRVFSVFLGSR-----AYPHF	896
QY	582	PAF---IDETLAAGAENIADRGADASDDFEGTYEWRHMSDVAAYFNL--DIENSE	636
DB	897	CAGHAVDTLLELGGERILKMGDELCGQEEAFRTWAKVFAACDVCVGDVNIK	956
QY	637	DNKSTLS-----LQFVDSADMP--LAKMH--GAFSTNVVASKELQOPGSA	681
DB	957	ANNSLISNDRSWKRNKFRFTFAEAPELTQGLSNVHKRYSAARLLSRNLQSPKSRST	1016
QY	682	RHLEIEL--PKEASYQEGDHLGVIPRYNVEGIVNRTARFGIDA---SQQIRLEAEK--	734
DB	1017	IFVRLHTNGSQELQYQPDHGLGVFPGNHEDLVNALLIERLE-DAPPVNMVKKVLEERNT	1075
QY	735	-----LAHLPLAKTVSVEELLQYVELODPVTRTOLRAMAAKTVCPPHKVEALLE-	785
DB	1076	ALGVISNWTDELRLPCTTFQAFKYLDITPTPTLQLOQFASLATSEKEKQRLVLSKG	1135
QY	786	KQAYKEQVLAKRLTLMLELEKYPACEMKFSEFIALLPSIRPRYSSISSSPRVDEKQASIT	845
DB	1136	LQYEEMKWKGNPTIVEVEEFPSTQMPATLLLTQLSLLQPRYSSISSSPDMYDVEHLT	1195
QY	846	VSVVSGEAWSGYGE-YKGIASNYLAELQEGDITCFISTPQSEFTLPKDPETPLIMVGP	904
DB	1196	VAIVSYTRDGEPIHHGVCSSWLNRIQADELVPCFVRGAPS-FHLPRNPQVPCILVGP	1254
QY	905	TGVAPRGFVQARK-OLKEQOSIGEALHFGCRSPHEDVLYQEELENAOSEGII-TLHT	962
DB	1255	TGAPRSFQQQOFDQIHKGMNCPMVLVFGCRQSKIDHIYREETLQAKNKGVFRELYT	1314
QY	963	AFSRMPNQPTYYQHVMEQDGKLI--ELLDQGAHFYICGDSQMAPAVETLMKSYADV	1020
DB	1315	AYSREDPKPKYQDILQELAESVYRALKEQGGHIVVCGDVTMAADVLA-KA-IQRIW	1373
QY	1021	HQVSEADARLWLOOLEEKGRYAKDVW	1046
DB	1374	GKLSAEDAGVFISRMRRDNRHEDIF	1399

RESULT 10

US-09-123-708-4  
 ; Sequence 4, Application US/09123708  
 ; Patent No. 6146887  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SCHRADER, Juergen  
 ; APPLICANT: GODECKE, Axel  
 ; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC  
 ; FILE REFERENCE: 511169-2003  
 ; CURRENT APPLICATION NUMBER: US/09/123,708  
 ; CURRENT FILING DATE: 1998-07-28  
 ; EARLIER APPLICATION NUMBER: 08/553,503  
 ; EARLIER FILING DATE: 1996-03-01  
 ; EARLIER APPLICATION NUMBER: P4411402.8  
 ; EARLIER FILING DATE: 1994-03-31  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 1433  
 ; TYPE: PRT  
 ; ORGANISM: Cytomegalovirus  
 ; US-09-123-708-4

QY	457	GIPSPSTEQSAKKVRKAE-----NAHNTPLLVLYGSMGTAGCTARDLADIA	504
DB	722	GTNGTPTKRAIGFKLAELAEVKSALMGQAMAKRVKATILYATETKSAQYAKTICEI-	780
QY	505	MSKGFAPQVATLDSH-AGNLPREGAVLIVTASY-NGHPPDNAKOF-----	547
DB	781	FKHAFDAKVMSEYDIVLHEHTLVIVTSTFGNGDPPENGKFGCALMEMRHPNSVQE	840
QY	548	-----VDWLQD-ASADEVKGVRYSVFGCGDKNNWATTYQKV	581
DB	841	ERKSYKVRFSVSYSDSKSGDGLDRNDFESAGPLANRVFSVFLGSR-----AYPHF	896
QY	582	PAF---IDETLAAGAENIADRGADASDDFEGTYEWRHMSDVAAYFNL--DIENSE	636
DB	897	CAGHAVDTLLELGGERILKMGDELCGQEEAFRTWAKVFAACDVCVGDVNIK	956
QY	637	DNKSTLS-----LQFVDSADMP--LAKMH--GAFSTNVVASKELQOPGSA	681
DB	957	ANNSLISNDRSWKRNKFRFTFAEAPELTQGLSNVHKRYSAARLLSRNLQSPKSRST	1016
QY	682	RHLEIEL--PKEASYQEGDHLGVIPRYNVEGIVNRTARFGIDA---SQQIRLEAEK--	734
DB	1017	IFVRLHTNGSQELQYQPDHGLGVFPGNHEDLVNALLIERLE-DAPPVNMVKKVLEERNT	1075
QY	735	-----LAHLPLAKTVSVEELLQYVELODPVTRTOLRAMAAKTVCPPHKVEALLE-	785
DB	1076	ALGVISNWTDELRLPCTTFQAFKYLDITPTPTLQLOQFASLATSEKEKQRLVLSKG	1135
QY	786	KQAYKEQVLAKRLTLMLELEKYPACEMKFSEFIALLPSIRPRYSSISSSPRVDEKQASIT	845
DB	1136	LQYEEMKWKGNPTIVEVEEFPSTQMPATLLLTQLSLLQPRYSSISSSPDMYDVEHLT	1195
QY	846	VSVVSGEAWSGYGE-YKGIASNYLAELQEGDITCFISTPQSEFTLPKDPETPLIMVGP	904
DB	1196	VAIVSYTRDGEPIHHGVCSSWLNRIQADELVPCFVRGAPS-FHLPRNPQVPCILVGP	1254
QY	905	TGVAPRGFVQARK-OLKEQOSIGEALHFGCRSPHEDVLYQEELENAOSEGII-TLHT	962
DB	1255	TGAPRSFQQQOFDQIHKGMNCPMVLVFGCRQSKIDHIYREETLQAKNKGVFRELYT	1314
QY	963	AFSRMPNQPTYYQHVMEQDGKLI--ELLDQGAHFYICGDSQMAPAVETLMKSYADV	1020
DB	1315	AYSREDPKPKYQDILQELAESVYRALKEQGGHIVVCGDVTMAADVLA-KA-IQRIW	1373
QY	1021	HQVSEADARLWLOOLEEKGRYAKDVW	1046



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QY 582 PAF---IDETLAAGAENIADRGADADDDFEGTYEWEHRHMWSDVAAYFNL--DIENSE 636
Db 897 CAFGHAVDTLLELGGERILKREGDELCOGEEAFRTWAKKVFKAACDVFVCGDDVNIK 956
QY 637 DNKSTLS-----LOFVDSAADMP--LAKMH--GAFSTNVVASKELQOPGSGARST 681
Db 957 ANNSLISNDRSWSKRNKFRLTFAVAEPELTQGLSNVHKRVSAARLLSRQLQSPKSSRST 1016
QY 682 RHEIELEL--PKEASYQEGDHLGVPYRNYEGIVNKTARFGLDA--SQOIRLEAEBEK-- 734
Db 1017 IFVRLHTNGSQELQYQDHLGVPYRNYEGIVNKTARFGLDA--SQOIRLEAEBEK-- 1075
QY 735 -----LAHLPLAKTVSVEELLQYVELOQDPTVTRTOLRAMAAKTVCPPHKEVEALLE- 785
Db 1076 ALGVISNWTDELPLPCTIFQAFKYLDITPTTLOQFASLATSEKEKQRLVLSKG 1135
QY 786 QKAYKEOVLAKRLTMELEKYPACEMKFSEFTALLPSIRPRYSISSSPRVDEKQASIT 845
Db 1136 LQYEWEKWKGNPTIVEVEEFPSTQMPATLLTQLSLQPRYSISSSPDMYDVEHLT 1195
QY 846 VSVVSGEAWSGYGE-YKGIASNYLAELQEGDTTCFISTPQSEFTTLPKDPTPLIMVGP 904
Db 1196 VAIVSYTRDGEPIHHGVCSWLNRIOADELVPCFVRGAPS-FHLPRNPQVPCILVGP 1254
QY 905 TGVAPEFGFVQARK-OLKEGQOSLGEAHLFGCRSPHEDLYOEBLENAOSEGII-TLHT 962
Db 1255 TGIAPFRSQOQFDIQQHGMNCPMVLVFGCRQSKIDHIYREETLQAKNKGVFRELYT 1314
QY 963 AFSRMPNQPTYYVQHVMEODGKKLI--ELLDDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 1315 AYSREDPKPKYVQDILQEQALAESVYRALKEQGHHYVCGDVTMAADVLA--IQRIWTOQ 1373
QY 1021 HQVSEADARLWLOOLEKGRYAKDVW 1046
Db 1374 GKLSAEDAGVFISMRDNRHEDIF 1399
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## RESULT 13

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US-08-365-486A-19
; Sequence 19, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1434 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-365-486A-19

Query Match 12.4%; Score 675; DB 2; Length 1434;
Best Local Similarity 28.0%; Pred. No. 4.9e-50;
Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

QY 457 GIPSPTEQSAKKVRKAE-----NAHNTPLLVLVYSGNMGTAECTARDLADIA 504
Db 723 GTNGTPTKRAIGFKLAEAVKFSKLMGOMAKRVKATILYATETKSOAYAKTLCGEI- 781
QY 505 MSKGFAFQATLDLASH-AGNLPREGAVLIVTASY-NGHPPDNNAKQF----- 547
Db 782 FKHAFAKVMSEEDYDIVLHEHETLVLVVSTFGNGDPPENGEKFGCALMEMRHPNSVQE 841
QY 548 -----VDWLDQ-ASADEVKGVRYSVFCGDKKNWATTVTKV 581
Db 842 ERKSYKVRFSVSYSDSKSGDGLDRDNFESAGFLANVRFVFGLSR-----AYPHF 897
QY 582 PAF---IDETLAAGAENIADRGADADDDFEGTYEWEHRHMWSDVAAYFNL--DIENSE 636
Db 898 CAFGHAVDTLLELGGERILKREGDELCOGEEAFRTWAKKVFKAACDVFVCGDDVNIK 957
QY 637 DNKSTLS-----LOFVDSAADMP--LAKMH--GAFSTNVVASKELQOPGSGARST 681
Db 958 ANNSLISNDRSWSKRNKFRLTFAVAEPELTQGLSNVHKRVSAARLLSRQLQSPKSSRST 1017
QY 682 RHEIELEL--PKEASYQEGDHLGVPYRNYEGIVNKTARFGLDA--SQOIRLEAEBEK-- 734
Db 1018 IFVRLHTNGSQELQYQDHLGVPYRNYEGIVNKTARFGLDA--SQOIRLEAEBEK-- 1076
QY 735 -----LAHLPLAKTVSVEELLQYVELOQDPTVTRTOLRAMAAKTVCPPHKEVEALLE- 785
Db 1077 ALGVISNWTDELPLPCTIFQAFKYLDITPTTLOQFASLATSEKEKQRLVLSKG 1136
QY 786 QKAYKEOVLAKRLTMELEKYPACEMKFSEFTALLPSIRPRYSISSSPRVDEKQASIT 845
Db 1137 LQYEWEKWKGNPTIVEVEEFPSTQMPATLLTQLSLQPRYSISSSPDMYDVEHLT 1196
QY 846 VSVVSGEAWSGYGE-YKGIASNYLAELQEGDTTCFISTPQSEFTTLPKDPTPLIMVGP 904
Db 1197 VAIVSYTRDGEPIHHGVCSWLNRIOADELVPCFVRGAPS-FHLPRNPQVPCILVGP 1255
QY 905 TGVAPEFGFVQARK-OLKEGQOSLGEAHLFGCRSPHEDLYOEBLENAOSEGII-TLHT 962
Db 1256 TGIAPFRSQOQFDIQQHGMNCPMVLVFGCRQSKIDHIYREETLQAKNKGVFRELYT 1315
QY 963 AFSRMPNQPTYYVQHVMEODGKKLI--ELLDDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
Db 1316 AYSREDPKPKYVQDILQEQALAESVYRALKEQGHHYVCGDVTMAADVLA--IQRIWTOQ 1374
QY 1021 HQVSEADARLWLOOLEKGRYAKDVW 1046
Db 1375 GKLSAEDAGVFISMRDNRHEDIF 1400
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## RESULT 14

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US-08-880-342-19
; Sequence 19, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	766	14.0	677	9	US-09-371-347-23	Sequence 23, Appl
2	705.5	12.9	588	10	US-09-765-873A-14	Sequence 14, App
3	675	12.4	1433	9	US-10-224-249-14	Sequence 14, Appl
4	665.5	12.2	1144	9	US-09-870-759-134	Sequence 124, App
5	650	11.9	1153	9	US-10-224-249-13	Sequence 13, Appl
6	650	11.9	1153	10	US-09-992-056-2	Sequence 2, Appl
7	608.5	11.2	1203	9	US-10-224-249-15	Sequence 15, Appl
8	598	11.0	679	9	US-10-138-838-117	Sequence 117, App
9	598	11.0	679	9	US-10-139-031-117	Sequence 117, App
10	598	11.0	679	9	US-10-138-905-117	Sequence 117, App
11	598	11.0	679	9	US-10-138-916-117	Sequence 117, App
12	598	11.0	679	9	US-09-976-800-117	Sequence 117, App
13	597	10.9	679	9	US-10-138-838-83	Sequence 83, Appl
14	597	10.9	679	9	US-10-139-031-83	Sequence 83, Appl
15	597	10.9	679	9	US-10-138-905-83	Sequence 83, Appl
16	597	10.9	679	9	US-10-138-916-83	Sequence 83, Appl
17	597	10.9	679	9	US-09-976-800-83	Sequence 83, Appl
18	594	10.9	679	9	US-10-138-838-118	Sequence 118, App
19	594	10.9	679	9	US-10-139-031-118	Sequence 118, App

Qy 609 FE

609 FEGTYEEWREHMSDVAAYFNLDIENSEDNKSTLSLQF---VDSA-----ANQY

212	Db	LEEDFTWREQFWPACVCHFGVEATGESSIRQYELVYVHTDIDAAKVMGEMGRLSYEN	271
660	QY	-----GAFSTNVASKELQOQCSARSTRHLEIEL-PKEASVQEGDHLGVTPRVEGI	710
272	Db	QPPDPDAKNPFLAAVTTNRKLNQ-GTERHLMHLELSDSKIRYESGDHVAVVPANDSAL	330
711	QY	VNRVTARFG--LDASQQIRLEAEFEKLAHLPLAKTVSVEELLQVVELODPTVTTQLRAMA	768
331	Db	VNOLAKKILGADUDVNVSNLNDENKHKHPPCPTSTRTALTYYLDITNP-PRTNVLYEL	389
769	QY	AKTVCPPHKVELEALLE-----KOAYKEOVIAKRLTMLELLEKYIPACEMKFSEFIALLP	822
390	Db	AQYASEPSEQELLRKMASSGEGELYLSWVVEARRHILAILQDQPSLRPPIDHLCCELLP	449
823	QY	SIRPRYISISSPRYDERQASITVYSWGSAWSGEYKGTASNYL-AELQEGDT-----	876
450	Db	RLQARYSISTASSKVHPNSVHCIAVVVEYETKAGRIN-KGVATVNLWRAKEPVGENGCRAL	508
877	QY	ITCFISTPQSEFTLPKDPETPLIMVGPCTGVAPRGFVQARKQLKQOGOSLGAHLYFGC	936
509	Db	VPMEYR--KSQFLRPFKATTPVIMVGPCTGVAPPIGFIOERAWLRQGRKEVGETLYLYCG	566
937	QY	RSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPTYYVQHYMEQDGKGLIELLDQGAH	995
567	Db	RRSDEDYLYRELAQFHRDGAULTQNVAFSREQSH-KVYVQHLLKQDREHLWKLIEGGAH	625
996	QY	FTYICGGSQMAPAVEATLMKSYADHVQVSEADARLWLOQLLEEKRYAKDVWA	1047
626	Db	IYVCQDARNMARDVONTFYDVAELGAMENHAQAVDYIKKLMTKGRYSLDWVS	677

RESULT 2

US-09-765-873A-14  
; Sequence 14, Application US/09765873A

; Patent No. US20010053

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: 004741
: GENERAL INFORMATION:
: APPLICANT: Tang, Xiao-Song
: TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
: FILE REFERENCE: BC1009 US CIP
: CURRENT APPLICATION NUMBER: US/09/765,873A
: CURRENT FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: US 09/627,216
: PRIOR FILING DATE: 2000-07-27
: PRIOR APPLICATION NUMBER: US 60/147,719
: PRIOR FILING DATE: 1999-08-06
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 14
: LENGTH: 588
: TYPE: PRT
: ORGANISM: Helianthus tuberosus
: US-09-765-873A-14

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Query Match	12.98;	Score	705.5;	DB	10;	Length	588;
Best Local Similarity	31.9%;	Pred. No.	1.8e-43;				
Matches	189;	Conservative	92;	Mismatches	245;	Indels	67;
Qy	499	DLADIAMSKGFAQVATLDSHAGNLPRGAVLIVTASY-N	NGHPDPAKQFVDWLDAQSAD	557			
Db	18	DLDYA-----ADDEYAKFKKETFAPFLATYGG	ETPDNARYKWFTEG---	65			
Qy	558	EVKG-----RYSVFGCGKNWATYQKVPAFIDT	LAAKGAENIADRGADASDDFEGT	612			
Db	66	DDKGVMLEKHVYVGLGNKQY-EHFNKIALVVD	EGLTEQAKRFYVPGLDGDDQSTEDD	124			
Qy	613	YEWREHWSDVAAAYFNLDIENSEDNKS-----	TLSL-----QFVDSADMDPL	655			
Db	125	FSAWKELVPDLQOLL-LD-----EDDKTAAT	PYTAAPYRVVPHDKPDTFSNHSQTNG	179			
Qy	656	AKMHA---FSTNVVASKELQOPGSARSTRHLE	IEIHPKEA-SYQEGDHLGLVIPRNYEGIV	711			
Db	180	HTVHDQAQPCRSNVAVKLEHTPESRSCPTHLE	FDTSHTGLSYETGHDVGVCIENLEVV	239			

QY	712	NRVTARFGLDASQIRLEAEAEKLAHL-----PLAKTVSVEELLOQVYELQDPVTRTOL	764
Db	240	EEAEKLI GLPADTYSFLHIDNEDGTPGLGGPTLQPPFPCTLRKALTNYADLLSSPKKSTL	299
QY	765	RAMAAKTVCPPHKHVELEALLE---KOAYKEQVLAIRLTMLELLEYKPCACMEFSEFI-AL	820
Db	300	LALAAHASDATEADRLQLASREGKDEYAEWVANQORSLLEVMEAFPSAKPLGVFFFAAI	359
QY	821	LPSITPRYYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKCIANSY-----LAELOQB	874
Db	360	APRLQPRYYSISSSPKMPVNRHIVTICALY-EKTPGGRHKGICSTWKNMKNVPLTENQDC	418
QY	875	DTITCFITPOSEFTLPKDPETPLIMVGPGTVAPFRGFQVARKOLKEQOQSIGLAHYF	934
Db	419	SSAIFVET--SNFKLPADPKVPVIMIGTGLAPFRGLQRLALKESGTELGOSILEFF	476
QY	935	GCRSPHEDLYQEELENASQSEGIT-LHTAFSRMPNQKTYVQHVMQDGKKLIELLDQG	993
Db	477	GCRNRKVDIFYENELNFFVENGALSELDMAFSR-EGASKEYVQHKMSQKASDIWNWLSG	535
QY	994	AHFYICGDSGOMAPAVEATLMKSYADVHQVSPADARLMLQOLEEGRYAKDWM	1046
Db	536	AYLYVCGDAKMAKDVTHTLHTIVQEOGNLDSSKAELEYVKNLOMSGSRLYRDVW	588

### RESULT 3

US-10-224-249-14  
; Sequence 14, Application US/10224249

; Publication No. US20

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Query Match	12.4%	Score 675;	DB 9;	Length 1433;
Best Local Similarity	28.0%;	Pred. No. 1.2e-40;		
Matches 192;	Conservative 132;	Mismatches 258;	Indels 104;	Gaps 23

	104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919
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QY 637 DNKSTLS-----LQFVDSAADMP--LAKMH--GAFSTNVASKELQOPGSAARST 681  
 DB 957 ANNSLISNDRSWKNNKRLFAPELTQGLSNVHKRYSAARLLSRONLQSPKSRST 1016  
 QY 682 RHLIEL--PREASYQGDHIGVTPRNYEGIVNRVTARFGLDA---SQOIRLEAEBE-- 734  
 DB 1017 IFVRLHTNGSOELQYQPCDHLGVFPNGHEDLVNALIERLE--DAPPVNMVQKVELLEBRNT 1075  
 QY 735 -----LAHLPLAKTVSVEELQYVELQDVPVTRTQLRAMAAKTVCPPHKVELEALLE- 785  
 DB 1076 ALGVISNWTDELRLPPCTIIFQAFKYLDITPTPLQLQFASLATESEKEKQRLLVLSKG 1135  
 QY 786 KQAYKEQVLAKRLTMELELLEKYPACEMKFSEFIALLPSIRPRYYSISSPRVDEKQASIT 845  
 DB 1136 LQYEENKWKGNPTIVELEBPSIQMPATLLQLSLQPRYYSISSSPDMYDVEHLT 1195  
 QY 846 VSVVSGEAWSGYGE-YGKIASNYLAELOEGDTICFTISTPOSETLTKPDPTPLIMVGP 904  
 DB 1196 VAIYSYTRDGEPIHHGVCSWLNRIQADELVPFCVRGAPS--FHLPRNPQVPCILVGP 1254  
 QY 905 TGVAPFGFVQARK-OLKEOGOSLGEAHLVFCRSPHEDLYQELENAOSEGII-TLHT 962  
 DB 1255 TGIAPFSFWQORFDTQHKMNCMPVLPVFCRQSKIDHIYREETLQAKNKGFRLEYIT 1314  
 QY 963 AFSRMPNPKTYVQVHMEQDGKKLI--ELLDOGAHFYICGDGSGMAPAVEATLMKSYADV 1020  
 DB 1315 AYSREPKPKYVQDILQELAESVYRALKEQGHHVYCGDVTMAADVKA-IQRIWTTQ 1373  
 QY 1021 HGVSEADARLWLOLEKGRYAKDV 1046  
 DB 1374 GKLSAEDAGVEISRMDNRYHEDIF 1399

RESULT 4  
 US-09-870-759-124  
 ; Sequence 124, Application US/09870759  
 ; Patent No. US20020177551A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TERMAN, David S  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
 ; FILE REFERENCE: 870759  
 ; CURRENT APPLICATION NUMBER: US/09/870,759  
 ; PRIOR FILING DATE: 2002-01-14  
 ; PRIOR APPLICATION NUMBER: US 60/208,128  
 ; PRIOR FILING DATE: 2000-05-30  
 ; NUMBER OF SEQ ID NOS: 166  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 124  
 ; LENGTH: 1144  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-870-759-124

Query Match 12.2%; Score 665.5; DB 9; Length 1144;  
 Best Local Similarity 31.6%; Pred. No. 4.2e-40;  
 Matches 191; Conservative 111; Mismatches 245; Indels 57; Gaps 25;

QY 484 VLYGSNNKTGTARTADIAMSGFAPOVATLDH-AGNLPREGAVLIVTASY-NGHPP 541  
 DB 535 VLFATETGKSALADLATL-FSYAFNTKVCVMDQYKASTLEEQLLLVWTSTFGNGDCP 593  
 QY 542 DNA---KQFVDWLDAQSADEKGVYSVFGCGDKNWTATYKVPF---IDETLAAGAE 595  
 DB 594 SNGQTLKSLFMLELN---HTRYAVFGLG-----SSWYQFCFAFHDDIDQKLSHLGAS 645  
 QY 596 NIADRGADSDDEFGYEEVREHWS-----DVAAYFNLDIENSEDNKSTLQ---F 646  
 DB 646 QLAPTGEGLSGQEDAFRSWAVQTFRAACETFDVRSKHHIIPKRTSNATWEPQYRL 705  
 QY 647 VDSADM-----PLAKMH--GAFSTNVASKELQOPGSAARST--HLEIPLKEASYQEGD 698  
 DB 706 IQSPEPLDLNRLALSIHAKNVFTMLKLSQONLQSEKSRRTLLVOLTFEGRGSPYLPG 765

QY 699 HLGVIPIRNYEGIVNRVTARFGLDA---SQOIRLEAEBE-----KLAHLPLAKTVSVEEL 749  
 DB 766 HLGIFPGNQALVQGIILERV-VDCPTPHQTVCLVLEDESQSYWYKDKRLP---PCSLSQ 821  
 QY 750 LQY-VELQDPVTRTQLRAMAAKTVCPPHKVELEALLEKQAYKEQVLAKRLTMELELLEKYP 808  
 DB 822 LTYELDTTPPTQLQHLKARFATDETDRQLEALCQPSYNDNKFSSNNPTFLVLEEF 881  
 QY 809 ACENKFSEFTALLPSIRPRYYSISSPRVDEKQASITVSVVSGEAWSGYGE-YGKIASNY 867  
 DB 882 SLHVPAAPLLSQLPILKPRYYSISSQDHTSEVHLTVAVVYTYTRDQGGPLHHGVCSW 941  
 QY 868 LAELOEGDTICFTISTPOSETLTKPDPTPLIMVGPVGFVQAR-KQLKEQGS 926  
 DB 942 IRNLKPDQVPCFVRS-VSGFQLEDPSPQICLIGPGTGIAFFRSFQQRHLDSQHKGLK 1000  
 QY 927 LGEAHLVFCRSPHEDLYQEL-ENAOSEGIIITLHTAFSRMPNPKTYVQVHME-QDGK 984  
 DB 1001 GGRMSLVFGCRHPEEDHLYQEEMQVRRKRVLFQVHTGYSLRPGKPKYVQDILQKQLAN 1060  
 QY 985 KLIELL--DOGAHFYICGDGSGMAPAVEATLMKSYADVHVSEADARLWLOLEKGRYA 1042  
 DB 1061 EVLSVLHGEQ--HLYICGD--VRMARDVATTLKLVATKLNLUSEQVEDYFFQLKSQRHY 1118  
 QY 1043 KDVM 1046  
 DB 1119 EDIF 1122

RESULT 5  
 US-10-224-249-13  
 ; Sequence 13, Application US/10224249  
 ; Publication No. US20030087867A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vogels, Ronald V.  
 ; TITLE OF INVENTION: Gene therapy for enhancing and/or inducing angiogenesis  
 ; FILE REFERENCE: 2183-5233US  
 ; CURRENT APPLICATION NUMBER: US/10/224,249  
 ; PRIOR FILING DATE: 2002-08-19  
 ; PRIOR APPLICATION NUMBER: PCI/NL00/00482  
 ; PRIOR FILING DATE: 2000-07-07  
 ; PRIOR APPLICATION NUMBER: EP 99202263.2  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: US 60/143,101  
 ; PRIOR FILING DATE: 1999-07-09  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 13  
 ; LENGTH: 1153  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CHAIN  
 ; LOCATION: (1)..(1153)  
 ; OTHER INFORMATION: Homo sapiens inducible nitric oxide synthase  
 US-10-224-249-13

Query Match 11.9%; Score 650; DB 9; Length 1153;  
 Best Local Similarity 30.3%; Pred. No. 5.9e-39;  
 Matches 195; Conservative 112; Mismatches 272; Indels 64; Gaps 22;

QY 447 KAKSKKIPLGIPSPSTEQSAKKYRKA-----ENAHNPTLLVLYSGNMGTABGT 496  
 DB 507 RPKREIPL-----KVLVRAVLFACMLMRKMTASRVRTILFATETKSEAL 553  
 QY 497 ARDLADTAMSGFAPOVATLDH-AGNLPREGAVLIVTASY-NGHPPDNAAQFVDWLDAQ 554  
 DB 554 AWDLGLAL-FSCAFNPKVVCMDKYRLSCLEERLLVTVTSTFGNGDCPGNGEKLSFLML 612  
 QY 555 SADEVKGVYSVFGCGDKNWTATYKVPF---IDETLAAGAEINADRGADSDDEFG 611



Best Local Similarity 26.7%; Pred. No. 7e-36;  
Matches 191; Conservative 115; Mismatches 254; Indels 155; Gaps 24;  
QY 454 PLGIPSPSTEQSAKKVKAEN-----AHNTPLLVYGSNMGTAEGTARDL 500  
Db 479 PWKSAAGGTTIKTKFEVAVNAKVASLMTGVMKRVKATILYKSGSETGRAQSAQOL 538  
QY 501 ADIAMSAGFAPQVATLDH-AGNLPREGAVLIVTASY-NGHPPDNKQFV----- 548  
Db 539 GRL-FKAFDPRVLCMDYDVVLEHETLVLTSTFPGNDGPPENGESFAALMEMSGPY 597  
QY 549 -----DW-----LDQASAEVKGVRYSVFGCGDKNW 574  
Db 598 NSSPRPEQHSYKIRFNSISCSPLVSSWRKRKRESNTDSAGALGTLRFVFGLSR-- 655  
QY 575 ATYQKVPAP--IDETLAAGAENTADRGAEADSDDECTYEENREHMSDVAAYENLD 631  
Db 656 --AYHFCAPARAVDTLREELGGERLLQLGQDELQCEBAFGWAQAQAACETFCV- 712  
QY 632 IENSEDNKSTL-----SLQFVDSAADMLAKMHGAFSTNVVAS 669  
Db 713 ---GEDAKAARADIFSPKRWKQRYRLSAQAEGLOLLPGLIHVHREKM---FQATIRSV 766  
QY 670 KELQPGQSARSTRHLETEL--PKEASVQEGDHLGVIIPRNYEGIVNRVTARFGLDASQOIR 727  
Db 767 ENLQSSKSTRATILVRDLDTGGQGLQYQPGDHIGVCPNRPGLVEALLSR----- 816  
QY 728 LEAEELKLAHLPLAKT--VSVEELQ-----YVELQDP 758  
Db 817 --VED-----PPAPTEPVAVEQLEKSGPGPPGWVRDPRLPCTLRQALTFDLTISP 868  
QY 759 VTRTQLRAMAAKTVCPHPKVELEAL-LEKQAYKEQVLAKRLTMLELEKYPACEMKFESEF 817  
Db 869 PSQOLLRLTLAEEPREQLEALSDPRYEKWKWFRCTPLLEVLQEPSPVALPAPLL 928  
QY 818 IALLPSIRPRYSSISSPRVDEKQASITVSVSGEAWSGYGE-YKGIASNYLAELQEGDT 876  
Db 929 LTQLPLQPRYSVSSAPSTHPGEIHITVAIVLARTQDGLGLHYGVCSTWLSQLKPGDP 988  
QY 877 ITCFISIPQSEFTLPKDPETPLIMVGPCTGVPAPRFGVQAR-KOLKEGOSLGEAHLYFG 935  
Db 989 VPCFIRGAPS-FRLPPDPSPILCVLPGCTGIAPRFGWQERLHDIESKGLQPPWTLVFG 1047  
QY 936 CRSPHEDYLOELENQAQSGII-TLHTAFSRMPNQKTYVQHVMEODGKKLIE---LLD 991  
Db 1048 CRCSQLDHLRYDEQNAQQRGVFGRVLTAFSREPDNPKTYVQDILRTELAAEVRHVLCE 1107  
QY 992 QGAHFYICGDSQMAPAVEATLMKSYADHVQVSEADARLWLQOLEEKGRYAKDWM 1046  
Db 1108 RG-HMFVCGDVT-MATNVLQTVQRIATATEGDMELDEAGDVIGVLRDQOQRYHEDIF 1160

RESULT 8  
US-10-138-838-117  
; Sequence 117, Application US/10138838  
; Publication No. US20030049821A1  
; GENERAL INFORMATION:  
; APPLICANT: Wilson, Ron C.  
; APPLICANT: Craft, David L.  
; APPLICANT: Eirich, Dudley  
; APPLICANT: Eshoo, Mark  
; APPLICANT: Madduri, Krishna M.  
; APPLICANT: Cornett, Cathy A.  
; APPLICANT: Brenner, Alfred A.  
; APPLICANT: Tang, Maria  
; APPLICANT: Loper, John C.  
; APPLICANT: Gleeson, Martin  
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
; TITLE OF INVENTION: P450 OXIDOREDUCTASE  
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF  
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO  
; FILE REFERENCE: 1010-16  
; CURRENT APPLICATION NUMBER: US/10/138,838

; CURRENT FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US/09/976,800  
; PRIOR FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 117  
; LENGTH: 679  
; TYPE: PRT  
; ORGANISM: CANDIDATROPICALIS  
; US-10-138-838-117  
Query Match 11.0%; Score 598; DB 9; Length 679;  
Best Local Similarity 27.2%; Pred. No. 1.8e-35;  
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;  
QY 430 ELDIKETLTLKPEGVVVKAASKKI---PLGGIPSPSTEQSAKKVKAENAHNTPLLV 485  
Db 5 KLDLYVITITVAVAAVYFAKQFLDQPDQDTGSLTDSGNSRDVLSLTKKNNKNT--LLL 62  
QY 486 YGSNMGTAEGTARDLADIAAMSK-CFAPQVATLDH---AGNLPREGAVLIVTASY-NGH 539  
Db 63 FGSOTGTAEYANKLSRELHSRFGKLTWADFADYDWDNFGDITEDILVFFIVATYGE 122  
QY 540 PPDNAKQFVMDLQASAEVKGVRYSVFGCGDKNMTYQKVPAP---IDETLAAGAEN 596  
Db 123 PTDNADEFHTWLTE-EADTILSTLKYTVFGLGN---STYEFNAIGRRKFDRLSEKGD 177  
QY 597 IADRGAEADSDDEFTGTYEE---WREHMSDVAAYFNLD----- 631  
Db 178 FAEYAE---GDGCTGLDEDFMAWKNDVFDALKNDLNFEEKELKYPNVKLTERRDLSAA 234  
QY 632 ---IENSEDNKSTLSLQFVDSAADMLAKMHGAFSTNVVASKELQPGQSARSTRHLETEL 688  
Db 235 DSQVSLGEPNKKYINSEGLDLTKG-PEDHTH-PYLARITETRELFES-SKORHCIVVEDI 291  
QY 689 PK-EASVQEGDHLGVIIPRNYEGIVNRVTARFGLDASQOIRLEAEE-EKLAHLPLAKTVSV 746  
Db 292 SESNLKTYTGDHLAIWPSNSDENIKQFAKCFGLEDKLDTVIELKALDSTYTIPTPTTY 351  
QY 747 EELQ-VVELQDPVTRTQLRAMAAKTVCPHPKVELEAL---EKOAYKEQVLAKRLTML 801  
Db 352 GAVIRHLEISGVPVSOFLLSIAG---FAPDEETKKAFTRLGGOKGFAAKVTRKKNFIA 408  
QY 802 ELL-----EKYPACEMKFESEFTLPSIRPRYSSISSPRVDEKQASITVSVSGEAWSGY 857  
Db 409 DALLYSSNNAWSDVPFEFLIENVPHTLTPRYSISS-SLSEKQLINVTAVVEAEERADG 467  
QY 858 GEYKGIASNYLAELQ-----EGDTITCFISTP-----QSEFTLPKDPET 896  
Db 468 RPTGVTVTNLLKNVEIVQNKTKGKPLVHYDLGSPRGKFNKFKLPVHVRNSFKLPKNSTT 527  
QY 897 PLIMVGPCTGVPAPRFGVQAR-KOLKEGOSLGEAHLYFGCRSPHEDYLOEE-LENAQSE 955  
Db 528 PVILIGPTGTVAPLURGFVRVQVQKNGVNVKTLPLFYGCRNSNEDFLYKQENAEYASVL 587  
QY 956 G-IITLHTAFSRMPNQKTYVQHVMEODGKKLIELLDQGAHFYICGDSQMAPAVEATLM 1014  
Db 588 GENFEMENAFSRQDPSKKVYVQDKILENSQLVHLLTEGALIYYCGDASRDVQTTIS 647  
QY 1015 KSVADHVQVSEADARLWLQOLEEKGRYAKDWM 1046  
Db 648 KIVAKSREISDKAAELVSKWQVQRYQEDVW 679

RESULT 9  
US-10-139-031-117  
; Sequence 117, Application US/10139031  
; Publication No. US20030049822A1  
; GENERAL INFORMATION:  
; APPLICANT: Wilson, Ron C.  
; APPLICANT: Craft, David L.  
; APPLICANT: Eirich, Dudley  
; APPLICANT: Eshoo, Mark

APPLICANT: Madduri, Krishna M.  
APPLICANT: Cornett, Cathy A.  
APPLICANT: Brenner, Alfred A.  
APPLICANT: Tang, Maria  
APPLICANT: Loper, John C.  
APPLICANT: Gleeson, Martin  
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
TITLE OF INVENTION: P450 OXIDOREDUCTASE  
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF  
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO  
FILE REFERENCE: 1010-16  
CURRENT APPLICATION NUMBER: US/10/139,031  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: US/09/976,800  
PRIOR FILING DATE: 2001-10-12  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 117  
LENGTH: 679  
TYPE: PRT  
ORGANISM: CANDIDATROPICALIS  
US-10-139-031-117

Query Match 11.0%; Score 598; DB 9; Length: 679;  
Best Local Similarity 27.2%; Pred. No. 1.8e-35;  
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

QY 430 ELDIKETLTKPEGFVVKAKSKK1-----PLGGIPSPSTEQSAKKYKKAENAHNTPLLV 485  
DB 5 KLDLYIIVLVVAAVFAKNQFLQPDQDTGFLNTDGSNSRDVLTSLKKNKNT--LLL 62

QY 486 YGSNMGTAEAGTARDLADIAISK-GFAPQVATLDH-----AGNLPREGAVLIIVTASY-NGH 539  
DB 63 FGSQTGTAEDYANKLSRELHSRGLKTMVADPADYDNDWDFGDTEDILVFFIVATYGE 122

QY 540 PPDNAKQFVDWLDOASADEVKGVYVFCGCKDNWATYQKVPAP---IDETLAAGAEN 596  
DB 123 PTDNADEFHTWLTE-EADTSLTKYTVFGLGN-----STYEFFNAIGRKFDRLSEKGGDR 177

QY 597 IADRGADASDDFEGTYEE---WREHMWSDVAAYFNLD----- 631  
DB 178 FAEYAE---GDDGTGTLDEDFMAWKDNVFDALKNLNFEEKELKYEPPNVKLTERRDLSA 234

QY 632 ---INSEDNKSTLSQFVDSAADPLAKMHGAFSTNVVASKELQOQPSARSTRHLEIEL 688  
DB 235 DSQVSLGEPNKKYINSEGDILTKG-PFDHHT-PYLARITETRELFSS-SKDRHCIIHVEFDI 291

QY 689 PK-EASYQEGDHLGVIIPRYEGIVNRTARFGLDASQOIRLEAEE-EKLAHLPLAKTVSV 746  
DB 292 SESNLKYTTGDHLAIPNSDENIKQFAKCFGLEDKLDTVIELKALDSTYITIPFPTPT 351

QY 747 EELLQ-YVELQDPVTRTQLRAMAAKTVCPPHKEVEALL-----EKOAYKEQVLAKRLTML 801  
DB 352 GAVIRHLEISGPSVRQFFLSIAG---FAPDETKKAFTRLGDKQOEFAAKVTRRKFNTA 408

QY 802 ELL-----EKYPACEMKFSEFIALLSIRPRYISISSPRVDEKQASITVSVVSGAWSY 857  
DB 409 DALLYSSNAPWSVDPFEFLIENPHLTPTRYISISS-SLSEKQLINVTAVVEAEEADG 467

QY 858 GEYKGIASNYLAELQ-----EGDTITCFITSP-----QSEFTLPKDPET 896  
DB 468 RPTGVVTVMLKNVLEQVKTGEKPLVHVDLSGPGKFKNFKLPVHVRNSKFLPKNSNT 527

QY 897 PLIMVPGTGVAPFRGFGVQARQKQEQSGEALHYFCGRSPHEDILYQEE-LENAOSE 955  
DB 528 PVILIGPGTVAPLGRFVRVQVQKNGVNVGKTLFLYGCNRNEDFLYKQEWAYASVL 587

QY 956 G-IITLHTAFSRMPNQPTVYOHVMEQDQKLIELLDQGAHYICGDSQMAPAYEATLM 1014  
DB 588 GENFEMAFNRQDPSKVKYVQDKILENSQLVHELLTEGAIIVVCGDSARMARDVQTIS 647

QY 1015 KSYADHVQSEADARLWLOOLEEKGRYAKDVW 1046

DB 648 KIVAKSREISDKAAELVKSWSKVQNRQEDVW 679

## RESULT 10

US-10-138-905-117  
Sequence 117, Application US/10138905  
Publication No. US20030068800A1

## GENERAL INFORMATION:

APPLICANT: Willson, Ron C.  
APPLICANT: Craft, David L.  
APPLICANT: Eirich, Dudley  
APPLICANT: Eshoo, Mark  
APPLICANT: Madduri, Krishna M.  
APPLICANT: Cornett, Cathy A.  
APPLICANT: Brenner, Alfred A.  
APPLICANT: Tang, Maria  
APPLICANT: Loper, John C.  
APPLICANT: Gleeson, Martin  
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
TITLE OF INVENTION: P450 OXIDOREDUCTASE  
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF  
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO  
FILE REFERENCE: 1010-16  
CURRENT APPLICATION NUMBER: US/10/138,905  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: US/09/976,800  
PRIOR FILING DATE: 2001-10-12  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 117  
LENGTH: 679  
TYPE: PRT  
ORGANISM: CANDIDATROPICALIS  
US-10-138-905-117

Query Match 11.0%; Score 598; DB 9; Length 679;

Best Local Similarity 27.2%; Pred. No. 1.8e-35;

Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

QY 430 ELDIKETLTKPEGFVVKAKSKK1-----PLGGIPSPSTEQSAKKYKKAENAHNTPLLV 485  
DB 5 KLDLYIIVLVVAAVFAKNQFLQPDQDTGFLNTDGSNSRDVLTSLKKNKNT--LLL 62

QY 486 YGSNMGTAEAGTARDLADIAISK-GFAPQVATLDH-----AGNLPREGAVLIIVTASY-NGH 539  
DB 63 FGSQTGTAEDYANKLSRELHSRGLKTMVADPADYDNDWDFGDTEDILVFFIVATYGE 122

QY 540 PPDNAKQFVDWLDOASADEVKGVYVFCGCKDNWATYQKVPAP---IDETLAAGAEN 596  
DB 123 PTDNADEFHTWLTE-EADTSLTKYTVFGLGN-----STYEFFNAIGRKFDRLSEKGGDR 177

QY 597 IADRGADASDDFEGTYEE---WREHMWSDVAAYFNLD----- 631  
DB 178 FAEYAE---GDDGTGTLDEDFMAWKDNVFDALKNLNFEEKELKYEPPNVKLTERRDLSA 234

QY 632 ---INSEDNKSTLSQFVDSAADPLAKMHGAFSTNVVASKELQOQPSARSTRHLEIEL 688  
DB 235 DSQVSLGEPNKKYINSEGDILTKG-PFDHHT-PYLARITETRELFSS-SKDRHCIIHVEFDI 291

QY 689 PK-EASYQEGDHLGVIIPRYEGIVNRTARFGLDASQOIRLEAEE-EKLAHLPLAKTVSV 746  
DB 292 SESNLKYTTGDHLAIPNSDENIKQFAKCFGLEDKLDTVIELKALDSTYITIPFPTPT 351

QY 747 EELLQ-YVELQDPVTRTQLRAMAAKTVCPPHKEVEALL-----EKOAYKEQVLAKRLTML 801  
DB 352 GAVIRHLEISGPSVRQFFLSIAG---FAPDETKKAFTRLGDKQOEFAAKVTRRKFNTA 408

QY 802 ELL-----EKYPACEMKFSEFIALLSIRPRYISISSPRVDEKQASITVSVVSGAWSY 857  
DB 409 DALLYSSNAPWSVDPFEFLIENPHLTPTRYISISS-SLSEKQLINVTAVVEAEEADG 467

QY 858 GEYKGIASNYLAELQ-----EGDTITCFITSP-----QSEFTLPKDPET 896  
DB 468 RPTGVVTVMLKNVLEQVKTGEKPLVHVDLSGPGKFKNFKLPVHVRNSKFLPKNSNT 527

QY 897 PLIMVPGTGVAPFRGFGVQARQKQEQSGEALHYFCGRSPHEDILYQEE-LENAOSE 955  
DB 528 PVILIGPGTVAPLGRFVRVQVQKNGVNVGKTLFLYGCNRNEDFLYKQEWAYASVL 587

QY 956 G-IITLHTAFSRMPNQPTVYOHVMEQDQKLIELLDQGAHYICGDSQMAPAYEATLM 1014  
DB 588 GENFEMAFNRQDPSKVKYVQDKILENSQLVHELLTEGAIIVVCGDSARMARDVQTIS 647

QY 1015 KSYADHVQSEADARLWLOOLEEKGRYAKDVW 1046

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Db 468 RPTGVVNTLKNVEIQVONKTEKPLVHYDLSGRGKFNKFLPVHVRNSFKLPKNSTT 527
Qy 897 PLIMVGPGTGVAPRGFVOARKOLKEQOSLGEAHLFGCRSPHEDYLYQEE--LENAQSE 955
Db 528 PVILIGPGTGVAPLGRFVRVQVQKNGVNGKTLFFYGCNRSNEDFLYKQEWAYASVL 587
Qy 956 G-IITLHTAFSRMPNQKTYVQHVMEODGKKLIELLDQGAHFYICGDSGOMAPAVEATLM 1014
Db 588 GENFEMFNATSRQDPKSKVYVQDKILENSQLVHELLTEGALIYVCGDASRMARDVQTTIS 647
Qy 1015 KSYADVHVQSEADARLWLQLEEKGRYAKDWM 1046
Db 648 KIVAKSREISDKAALVKSMKVQNRQYQEDVM 679

RESULT 11
US-10-138-916-117
; Sequence 117, Application US/10138916
; Publication No. US20030073220A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Eirich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CYTOCHROME P450
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,916
; CURRENT FILING DATE: 2002-05-03
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/302,602
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-10-138-916-117

Query Match 11.0%; Score 598; DB 9; Length 679;
Best Local Similarity 27.2%; Pred. No. 1.8e-35;
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

Qy 430 ELDIKETITLKPEGFVVVAKSKKI----PLGGIPSPTEQSAKKVRKKAENAHNTPLLYL 485
Db 5 KLDLYVIITLVVAAYAFKNOFLDQPDQDTGFLNTDSGNSRDVLTSLTKNNKNT--LLL 62
Qy 486 YGSNMGTAEGTARDLADTAMSK-GFAPQVATLDSH----AGNLREGAVLIVTASY-NGH 539
Db 63 FGSOTGTAEDYANKLSRELHRSFGLKTMVADFADYDWDNFDGIDITDILVFFVATYGE 122
Qy 540 PPDNAKQFVMDQASADEVKGVRYSGCGDKNWTATYQKVPAP----IDETLAAGAEN 596
Db 123 PTDNADEFTWLT-EADTLSTLKYTVFGLGN----STYEFNAIGRKFRLLEKGGDR 177
Qy 597 IADRGEDASDDFGTVEE----WREHWSVAAVFNLD----- 631
Db 178 FAEYAE---GDGTGTLDDEPFMAWKDNVFDALKNDLNFEEKELYEPNVKLTERRDLSAA 234
Qy 632 ---TENSEDNKSTLSLOFVSAADMPLAKMHGAFSTNNVASKELQQPCGARSRTHLETEL 688
Db 235 DSQVSLGEPNKKYINSEGDITLTKG-PFDHTH-PYLARITETRELFS-SKDRCHLHVEFDI 291
Qy 689 PK-EASYOEGDHLGVIPRNTYEGIVNRVTAFFGLDASQOIRLEAEE-EKLAHLPLAKTVSV 746
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Db 292 SESNLKVTGTHLAIWPSNDSNENIKQFAKCFGLDKLDTVIELKALDSTYTPPTPTTY 351
Qy 747 EELLQ-YVELQDPVTRTQLRAMAAKTVCPPHKHVEALL----EKQAYKEQVLAKRLTML 801
Db 352 GAVIRHLEISGPPVSROFFLSIAG---FAPDEETKKAFTRLGSGDKQEFPAKVTRKFNIA 408
Qy 802 ELL----EKYPACEMKFSEFTALLPSIRPRYSISSSSPRVDEKQASIVSVSGEAWSGY 857
Db 409 DALLYSSNNAWPSDVPEFFLIENVPHLTTPRYSISSS-SLSEKQLINVTAVVEAEADG 467
Qy 858 GEYKGIASNYLAELQ-----EGDTITCTFISTP-----OSEFTLPKDPET 896
Db 468 RPTGVVNTLKNVEIQVONKTEKPLVHYDLSGRGKFNKFLPVHVRNSFKLPKNSTT 527
Qy 897 PLIMVGPGTGVAPRGFVOARKOLKEQOSLGEAHLFGCRSPHEDYLYQEE--LENAQSE 955
Db 528 PVILIGPGTGVAPLGRFVRVQVQKNGVNGKTLFFYGCNRSNEDFLYKQEWAYASVL 587
Qy 956 G-IITLHTAFSRMPNQKTYVQHVMEODGKKLIELLDQGAHFYICGDSGOMAPAVEATLM 1014
Db 588 GENFEMFNATSRQDPKSKVYVQDKILENSQLVHELLTEGALIYVCGDASRMARDVQTTIS 647
Qy 1015 KSYADVHVQSEADARLWLQLEEKGRYAKDWM 1046
Db 648 KIVAKSREISDKAALVKSMKVQNRQYQEDVM 679

RESULT 12
US-09-976-800-117
; Sequence 117, Application US/09976800
; Publication No. US20030077795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Eirich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CYTOCHROME P450
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976,800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-09-976-800-117

Query Match 11.0%; Score 598; DB 9; Length 679;
Best Local Similarity 27.2%; Pred. No. 1.8e-35;
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

Qy 430 ELDIKETITLKPEGFVVVAKSKKI----PLGGIPSPTEQSAKKVRKKAENAHNTPLLYL 485
Db 5 KLDLYVIITLVVAAYAFKNOFLDQPDQDTGFLNTDSGNSRDVLTSLTKNNKNT--LLL 62
Qy 486 YGSNMGTAEGTARDLADTAMSK-GFAPQVATLDSH----AGNLREGAVLIVTASY-NGH 539
Db 63 FGSOTGTAEDYANKLSRELHRSFGLKTMVADFADYDWDNFDGIDITDILVFFVATYGE 122
Qy 540 PPDNAKQFVMDQASADEVKGVRYSGCGDKNWTATYQKVPAP----IDETLAAGAEN 596
Db 123 PTDNADEFTWLT-EADTLSTLKYTVFGLGN----STYEFNAIGRKFRLLEKGGDR 177
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QY 597 IADRGADASDDFEGTYEE-----WREHMDSVAAAYFNLD----- 631  
Db 178 FAEYAE---GDDGTGLDDEFMAWKONVFDALKNDLNFEEKELKYPNVKLTERRDLSAA 234  
QY 632 ---IENSEDNKSTLSQFVDSADMLAKMHGAFSTNVVASKELQPGQSGARSTRHLEIEL 688  
Db 235 DSQVSLGEPNKKYINSEGDILTKG-PFDHHT-PYLARITETRELF-SKDRHCIHVEFDI 291  
QY 689 PK-EASYQEGDHLGVIIPRYEGIVNRVTRARFGLDASQOIRLEAEE-EKLAHLPLAKTVSV 746  
Db 292 SESNLKYYTGDHLAIWPSNSDENIKQFAKFCGLEDKLDVIELKALDSTYTPFPPIY 351  
QY 747 EELLO-YVELOQPVTRTQIRAMAATVCPHPKVELEALL-----EKQAYKEQVLAKRLTML 801  
Db 528 PVILIGTGTGAPLRGFRVRRVQVQKNGVNVGKTLFLFYGRNSNEDELYKQWAEYASVL 587  
QY 956 G-IITLHTAFSRMPNPKTYVOHVMEQDGKLELDDOGAHEFYICGDSQMAPAVEATLM 1014  
Db 588 GENFEMFASRODPSKKYIVQDKILENSOLVHELITGAILIYVCGDSARMARDVQTTIS 647  
QY 1015 KSYADYHVQSEADARLWLOOLEKGRYAKDVW 1046  
Db 648 KIVAKSREISEDKAELVKSWKVQRYQEDVW 679

## RESULT 13

US-10-138-838-83  
; Sequence 83, Application US/10138838  
; Publication No. US20030049821A1  
; GENERAL INFORMATION:  
; APPLICANT: Wilson, Ron C.  
; APPLICANT: Craft, David L.  
; APPLICANT: Eirich, Dudley  
; APPLICANT: Eshoo, Mark  
; APPLICANT: Madduri, Krishna M.  
; APPLICANT: Cornett, Cathy A.  
; APPLICANT: Brenner, Alfred A.  
; APPLICANT: Tang, John C.  
; APPLICANT: Gleeson, Martin  
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
; TITLE OF INVENTION: P450 OXIDOREDUCTASE  
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF  
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO  
; FILE REFERENCE: 1010-16  
; CURRENT APPLICATION NUMBER: US/10/138,838  
; CURRENT FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US/09/976,800  
; PRIOR FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 83  
; LENGTH: 679  
; TYPE: PRT  
; ORGANISM: CANDIDATROPICALIS  
US-10-138-838-83

Query Match 10.9%; Score 597; DB 9; Length 679;  
Best Local Similarity 27.2%; Pred. No. 2.1e-35;  
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

QY 430 ELDIKETLTKPEGFVYVAKRSKKI-----PLGGIPSPSTBQSAKKVKKKAENAHTLPLVL 485  
Db 5 KLDLYIITLVAVAAAFKFNQFLDQPDQDTGFLNTDGSNSRDVLLTLAKNNKNT--LLL 62  
QY 486 YSNMGTAAGTARDLADIAMSK-GFAPQVATLDH-----AGNLPRGAVLIVTASY-NGH 539  
Db 63 FGSQTGAEDYANKLSRELHSRFLGKTMVADFADYDWNDFGDTIDILVFFIVATYGE 122  
QY 540 PDNAKQFVDVLDASADEKGVYRVSVFGCGDKNWTATYQKPAF---IDETLAAGAEN 596  
Db 123 PDNADEFHTWTE-EADTLSTLTKYTVFGLGN-----STYEFFNAIGKFRDLLEKGGOR 177  
QY 597 IADRGADASDDFEGTYEE-----WREHMDSVAAAYFNLD----- 631  
Db 178 FAEYAE---GDDGTGLDDEFMAWKONVFDALKNDLNFEEKELKYPNVKLTERRDLSAA 234  
QY 632 ---IENSEDNKSTLSQFVDSADMLAKMHGAFSTNVVASKELQPGQSGARSTRHLEIEL 688  
Db 235 DSQVSLGEPNKKYINSEGDILTKG-PFDHHT-PYLARITETRELF-SKDRHCIHVEFDI 291  
QY 689 PK-EASYQEGDHLGVIIPRYEGIVNRVTRARFGLDASQOIRLEAEE-EKLAHLPLAKTVSV 746  
Db 292 SESNLKYYTGDHLAIWPSNSDENIKQFAKFCGLEDKLDVIELKALDSTYTPFPPIY 351  
QY 747 EELLO-YVELOQPVTRTQIRAMAATVCPHPKVELEALL-----EKQAYKEQVLAKRLTML 801  
Db 352 GAVIRHLEISGVPVSQRFLLSIAG---FAPDEETKKAFTRLGGDKQFAAKVTRRRFNIA 408  
QY 802 ELL-----EKYPACEMKFEFIALLSIRPRYYSISSPRVDEKQASITVSVYSGEAWSGY 857  
Db 409 DALLYSSNAPWSVDFEFLIENPHLTIPRYYSISS-SLSEKQLINVTAVVEAEADG 467  
QY 858 GEYKGIASNYLAELQ-----EGDTITCFISTP-----OSETPLPKDPET 896  
Db 468 RPYTGVTNLLKNNVEIVQNKTEKPLVHYDLSGPRGKFNKFLPVHVRSRNFKLPKNSYT 527  
QY 897 PLIMVPGTGVAPFRGVOARKQKQOSLGEAHLFYGCRSPHEDLYQEE-LENAQSE 955  
Db 528 PVILIGTGTGAPLRGFRVRRVQVQKNGVNVGKTLFLFYGRNSNEDELYKQWAEYASVL 587  
QY 956 G-IITLHTAFSRMPNPKTYVOHVMEQDGKLELDDOGAHEFYICGDSQMAPAVEATLM 1014  
Db 588 GENFEMFASRODPSKKYIVQDKILENSOLVHELITGAILIYVCGDSARMARDVQTTIS 647  
QY 1015 KSYADYHVQSEADARLWLOOLEKGRYAKDVW 1046  
Db 648 KIVAKSREISEDKAELVKSWKVQRYQEDVW 679

## RESULT 14

US-10-139-031-83  
; Sequence 83, Application US/10139031  
; Publication No. US20030049822A1  
; GENERAL INFORMATION:  
; APPLICANT: Wilson, Ron C.  
; APPLICANT: Craft, David L.  
; APPLICANT: Eirich, Dudley  
; APPLICANT: Eshoo, Mark  
; APPLICANT: Madduri, Krishna M.  
; APPLICANT: Cornett, Cathy A.  
; APPLICANT: Brenner, Alfred A.  
; APPLICANT: Tang, John C.  
; APPLICANT: Gleeson, Martin  
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
; TITLE OF INVENTION: P450 OXIDOREDUCTASE  
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF  
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO  
; FILE REFERENCE: 1010-16  
; CURRENT APPLICATION NUMBER: US/10/139,031  
; CURRENT FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US/09/976,800  
; PRIOR FILING DATE: 2001-10-12

; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 83  
; LENGTH: 679  
; TYPE: PRT  
; ORGANISM: CANDIDATROPICALIS  
; US-10-139-031-83

Query Match 10.9%; Score 597; DB 9; Length 679;  
Best Local Similarity 27.2%; Pred. No. 2.1e-35;  
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;  
QY 430 ELDIKETLTKPEGFYVVKAKSKKI-----PLGGIPSPSTEQSAKKVKKKAENAHNTPLLV 485  
Db 5 KLDLYIITLVAVAAAFKQFLDQPDGTGFLNTDGSNSRDVLLTLKNNKNT--LLL 62  
QY 486 YGSNMGTAEGTARDLADIAMSK-GFAPQVATLDH-----AGNLPREGAVLIVTASY-NGH 539  
Db 63 FGSQTGAEDYANKLSRELHSRGLKTMVADFADYDWNFGDITDILVFFIVATYGE 122  
QY 540 PPDNAQFVDWLDOASADEVKGVYSVFGGDKNWTATYKVPF--IDETLAAGAEN 596  
Db 123 PTDNADEFHTLWTE-RADTLSTLKYTVFGLGN-----STYEFFNAIGRKFDRLLSEKGGDR 177  
QY 597 IADRGADASDDPEGTYEE-----WREHMWSVAAAYFNLD----- 631  
Db 178 FAEYAE---GDDGTGTLDEDFMAWKDNVFDALKNDLNFEEKELKYPNVKLTERRDLSAA 234  
QY 632 ---IENSEDNKSTLSLQFVDSADMPKMHGAFSTNVVASKELQPGSARSTRHLEIEL 688  
Db 235 DSQVSLGEPNKKYINSEGIDLTGK-PFDHHT-PYLARITETRELFSS-KDRHCHIHVEFDI 291  
QY 689 PK-EASYQEGDHLGVIPRNVYEGIVNRTARFGLDASQOIRLEAEE-EKLAHLPLAKTVSV 746  
Db 292 SESNLAYTTGDHLAIWPSNSDENIKQFAKFCGLEDKLDTVIELKALDSTYTFPPPIY 351  
QY 747 EELLQ-YVELQDPVTRTQLRAMAAKTVCPPHKVLEALL-----EKQAYKEQVLAKRLTML 801  
Db 352 GAVIRHLEITSGPVSRQFLSIAG---FAPDEETKKAFTRLGGDKQFAAKVTRRKNFNA 408  
QY 802 ELL-----EKYPACEMKFSEFIALPSIRPRYISISSPRVDEKQASITVSVSGEAWSGY 857  
Db 409 DALLYSSNAPWSVDPFEFLIENVPHLTPRYISISS-SLSEKQLINVTAVVEAEADG 467  
QY 858 GEYKGIASNYLAELQ-----EGDITTCFISPP-----OSEFTLPKDPET 896  
Db 468 RPYTGVTNLLKNVEIVONKTGKPLVHYDLSGPRGKFNKFLPVHVRNSFNKLPKNSIT 527  
QY 897 PLIMVPGTGVAPFRGFVQARKOLKEGOSLGBAHLYFGCRSPHEDYLYQEE-LENAQSE 955  
Db 528 PVILIGPGTGVAPLRGFRVQVKNVGNVGTLLFYGCGRNEDFLYKQWAEYASVL 587  
QY 956 G-LITLHTAFSRMPNPKTYVQHVMBQDGKLLLELDQGAHFYICGDSQMAPAVEATLM 1014  
Db 588 GENFEMNFAFSRODPSKKVYVDKILENSOLVHELLTEGAIIVYCGDASRMARDVQTTIS 647  
QY 1015 KSYADVHQVSEADARLWLOOLEKGRIKDVW 1046  
Db 648 KIVAKSREISEDKAELVSKWQVQRYQEDVW 679

## RESULT 15

US-10-138-905-83  
; Sequence 83, Application US/10138905  
; Publication No. US20030068800A1  
; GENERAL INFORMATION:  
; APPLICANT: Wilson, Ron C.  
; APPLICANT: Craft, David L.  
; APPLICANT: Eirich, Dudley  
; APPLICANT: Eshoo, Mark  
; APPLICANT: Madduri, Krishna M.  
; APPLICANT: Cornett, Cathy A.  
; APPLICANT: Brenner, Alfred A.

; APPLICANT: Tang, Maria  
; APPLICANT: Loper, John C.  
; APPLICANT: Gleeson, Martin  
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
; TITLE OF INVENTION: P450 OXIDOREDUCTASE  
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX O  
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO  
; FILE REFERENCE: 1010-16  
; CURRENT APPLICATION NUMBER: US/10/138,905  
; CURRENT FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US/09/976,800  
; PRIOR FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 83  
; LENGTH: 679  
; TYPE: PRT  
; ORGANISM: CANDIDATROPICALIS  
; US-10-138-905-83

Query Match 10.9%; Score 597; DB 9; Length 679;  
Best Local Similarity 27.2%; Pred. No. 2.1e-35;  
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;  
QY 430 ELDIKETLTKPEGFYVVKAKSKKI-----PLGGIPSPSTEQSAKKVKKKAENAHNTPLLV 485  
Db 5 KLDLYIITLVAVAAAFKQFLDQPDGTGFLNTDGSNSRDVLLTLKNNKNT--LLL 62  
QY 486 YGSNMGTAEGTARDLADIAMSK-GFAPQVATLDH-----AGNLPREGAVLIVTASY-NGH 539  
Db 63 FGSQTGAEDYANKLSRELHSRGLKTMVADFADYDWNFGDITDILVFFIVATYGE 122  
QY 540 PPDNAQFVDWLDOASADEVKGVYSVFGGDKNWTATYKVPF--IDETLAAGAEN 596  
Db 123 PTDNADEFHTLWTE-RADTLSTLKYTVFGLGN-----STYEFFNAIGRKFDRLLSEKGGDR 177  
QY 597 IADRGADASDDPEGTYEE-----WREHMWSVAAAYFNLD----- 631  
Db 178 FAEYAE---GDDGTGTLDEDFMAWKDNVFDALKNDLNFEEKELKYPNVKLTERRDLSAA 234  
QY 632 ---IENSEDNKSTLSLQFVDSADMPKMHGAFSTNVVASKELQPGSARSTRHLEIEL 688  
Db 235 DSQVSLGEPNKKYINSEGIDLTGK-PFDHHT-PYLARITETRELFSS-KDRHCHIHVEFDI 291  
QY 689 PK-EASYQEGDHLGVIPRNVYEGIVNRTARFGLDASQOIRLEAEE-EKLAHLPLAKTVSV 746  
Db 292 SESNLAYTTGDHLAIWPSNSDENIKQFAKFCGLEDKLDTVIELKALDSTYTFPPPIY 351  
QY 747 EELLQ-YVELQDPVTRTQLRAMAAKTVCPPHKVLEALL-----EKQAYKEQVLAKRLTML 801  
Db 352 GAVIRHLEITSGPVSRQFLSIAG---FAPDEETKKAFTRLGGDKQFAAKVTRRKNFNA 408  
QY 802 ELL-----EKYPACEMKFSEFIALPSIRPRYISISSPRVDEKQASITVSVSGEAWSGY 857  
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QY 858 GEYKGIASNYLAELQ-----EGDITTCFISPP-----OSEFTLPKDPET 896  
Db 468 RPYTGVTNLLKNVEIVONKTGKPLVHYDLSGPRGKFNKFLPVHVRNSFNKLPKNSIT 527  
QY 897 PLIMVPGTGVAPFRGFVQARKOLKEGOSLGBAHLYFGCRSPHEDYLYQEE-LENAQSE 955  
Db 528 PVILIGPGTGVAPLRGFRVQVKNVGNVGTLLFYGCGRNEDFLYKQWAEYASVL 587  
QY 956 G-LITLHTAFSRMPNPKTYVQHVMBQDGKLLLELDQGAHFYICGDSQMAPAVEATLM 1014  
Db 588 GENFEMNFAFSRODPSKKVYVDKILENSOLVHELLTEGAIIVYCGDASRMARDVQTTIS 647  
QY 1015 KSYADVHQVSEADARLWLOOLEKGRIKDVW 1046  
Db 648 KIVAKSREISEDKAELVSKWQVQRYQEDVW 679

Search completed: May 29, 2003, 08:27:08  
Job time : 35 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:22:12 ; Search time 163 Seconds  
(without alignments)  
4145.278 Million cell updates/sec

Title: US-10-031-146-2  
Perfect score: 5457  
Sequence: 1 TIKEMPOKTFGELKNLPL.....RLWLOLEKGRYAKVDWAG 1048

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents\_AA\_Main.\*

- 1: /cgn2\_6/ptodata/1/paa/PTCTUS\_COMB.pep.\*
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- 3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep.\*
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- 27: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5457	100.0	1048	24	US-10-031-146-2
2	5457	100.0	1048	24	US-10-031-241-35
3	5457	100.0	1048	24	US-10-031-695-2
4	5457	100.0	1049	1	PCT-US02-11954-2
5	5457	100.0	1049	21	US-09-791-537-53927
6	5457	100.0	1049	24	US-10-031-146-9

7	5457	100.0	1049	25	US-10-125-640-2
8	5457	100.0	1049	26	US-10-201-213-2
9	5449	99.9	1049	22	US-09-856-339A-21
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19	3281.5	60.1	1054	25	US-10-125-640-4
20	3281.5	60.1	1054	25	US-10-125-640-5
21	2466	45.2	471	21	US-09-791-537-94076
22	2461	45.1	471	21	US-09-791-537-71271
23	2429	44.5	464	1	PCT-US02-11954-3
24	2429	44.5	464	25	US-10-125-640-3
25	2402	44.0	458	21	US-09-791-537-116499
26	2386	43.7	455	21	US-09-791-537-8264
27	1736.5	31.8	1066	1	PCT-US02-11954-9
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29	1736.5	31.8	1066	25	US-10-125-640-9
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34	1002	18.4	191	21	US-09-791-537-116501
35	961	17.6	527	1	PCT-US02-11954-8
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41	777.5	14.2	678	21	US-09-791-537-10974
42	777.5	14.2	678	24	US-10-021-425-54
43	777.5	14.2	686	21	US-09-791-537-12987
44	775.5	14.2	678	21	US-09-791-537-56962
45	775	14.2	678	21	US-09-791-537-118779

ALIGNMENTS

RESULT 1

US-10-031-146-2  
; Sequence 2, Application US/10031146  
; GENERAL INFORMATION:  
; APPLICANT: HAUER, Bernhard  
; APPLICANT: PLEISS, Juergen  
; APPLICANT: SCHWANEBERG, Ulrich  
; APPLICANT: SCHMITT, Jutta  
; TITLE OF INVENTION: Novel cytochrome P450 monooxygenases and their use for the ox  
; TITLE OF INVENTION: organic substrates  
; FILE REFERENCE: 50915  
; CURRENT APPLICATION NUMBER: US/10/031.146  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: PCT/EP 00/07253  
; PRIOR FILING DATE: 2000-07-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Word Perfect version 6.1  
; SEQ ID NO 2  
; LENGTH: 1048  
; TYPE: PRT  
; ORGANISM: Bacillus megaterium  
US-10-031-146-2

Query Match 100.0%; Score 5457; DB 24; Length 1048;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPFSQOAMGYHAMV 120  
QY 121 DIAVLQVQWERLNADEHIEVPEDMTFLTDITGLGCFNYRFSFYRQDPHPITSMVRA 180  
Db 121 DIAVLQVQWERLNADEHIEVPEDMTFLTDITGLGCFNYRFSFYRQDPHPITSMVRA 180  
QY 181 LDEAMNKLQANPDPPAYDENKRFQEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 240  
Db 181 LDEAMNKLQANPDPPAYDENKRFQEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 240  
QY 241 KDPETGEPLDDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHVLOKAAEAARVLD 300  
Db 241 KDPETGEPLDDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHVLOKAAEAARVLD 300  
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Db 301 PVPYSYQVQKLVGVGNVLEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDDELWVLPOL 360  
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Db 361 HRDKTWGDVVEEFRPERFENPSAIPQHAFKPFNGQORACIGQOQFALHEATLVLGWMLKH 420  
QY 421 FDFEDHTNYELDIKETLTKPEGVYVKAASKKIPLGGIPSPSTEQSAKKVKAENAHNT 480  
Db 421 FDFEDHTNYELDIKETLTKPEGVYVKAASKKIPLGGIPSPSTEQSAKKVKAENAHNT 480  
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Db 481 PLLVLYGSGNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540  
QY 541 PDNAKQFVWLDOASADEVKGVYRYSVFGCGDKNWTYQKVPFADITETLAAGAENIADR 600  
Db 541 PDNAKQFVWLDOASADEVKGVYRYSVFGCGDKNWTYQKVPFADITETLAAGAENIADR 600  
QY 601 GEADASDDFEGTYEENREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 660  
Db 601 GEADASDDFEGTYEENREHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPPLAKMHG 660  
QY 661 AFSTNVVASKELQOQPGSARSTRHLEITELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720  
Db 661 AFSTNVVASKELQOQPGSARSTRHLEITELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720  
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Db 781 EALLERQAYKEQVLAERLTMLELLEKYPACEMKFSEFIALLPISIRPRYYSISSPRVDEK 840  
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RESULT 2

US-10-031-241-35

; Sequence 35, Application US/10031241  
; GENERAL INFORMATION:  
; APPLICANT: Hauer, Bernhard  
; APPLICANT: Schmid, Rolf D.  
; APPLICANT: Schwaneberg, Ulrich  
; TITLE OF INVENTION: Electron donor system for enzymes and its use in the biochemic  
; TITLE OF INVENTION: conversion of substrates  
; FILE REFERENCE: M/40076  
; CURRENT APPLICATION NUMBER: US/10/031,241  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP00/07251  
; PRIOR FILING DATE: 2000-07-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 1048  
; TYPE: PRT  
; ORGANISM: Bacillus megaterium  
; US-10-031-241-35

Query Match 100.0%; Score 5457; DB 24; Length 1048;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 DIAVLQVQWERLNADEHIEVPEDMTFLTDITGLGCFNYRFSFYRQDPHPITSMVRA 180  
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Db 181 LDEAMNKLQANPDPPAYDENKRFQEDIKVMNDLVDKIIADRKASGEQSDLLTHMLNG 240  
QY 241 KDPETGEPLDDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHVLOKAAEAARVLD 300  
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Db 961 HTAFSRMPNPKTYVQHVMEQDGKKLIELLDQGAHFYICGDSOMAPAVEATLMKSYADV 1020
QY 1021 HOVSEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1021 HOVSEADARLWLOOLEEKGRYAKDVWAG 1048
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## RESULT 3

US-10-031-695-2

; Sequence 2, Application US/10031695

; GENERAL INFORMATION:

; APPLICANT: Hauer, Bernhard

; APPLICANT: Pleiss, Jurgen

; APPLICANT: Schwaneberg, Ulrich

; APPLICANT: Schmitt, Jutta

; TITLE OF INVENTION: Modified cytochrome P450 monooxygenases

; FILE REFERENCE: M/40434

; CURRENT APPLICATION NUMBER: US/10/031.695

; PRIOR FILING DATE: 2002-05-06

; PRIOR APPLICATION NUMBER: PCT/EP00/07252

; PRIOR FILING DATE: 2000-07-27

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 1048

; TYPE: PRT

; ORGANISM: Bacillus megaterium

; US-10-031-695-2

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Query Match 100.0%; Score 5457; DB 24; Length 1048;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 ACDESREDKLSQALKVRFVDFAGDGLFTSWTHEKNWKAHNNILLPSFSQAMKGYHAMV 120
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Db 121 DIAVOLQVKWERLNADSHIEVPEDMTRLTLDITGLCGFNFRNSFYRDQHPFTTSMVRA 180
QY 181 LDEAMNKLQANPPDPAYDENKRFQEDIKVMNDLVKIIADRKASGEQSDLLTHMLNG 240
Db 181 LDEAMNKLQANPPDPAYDENKRFQEDIKVMNDLVKIIADRKASGEQSDLLTHMLNG 240
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Db 241 KDPETGEPDLDENTRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 300
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Db 421 FDFEDHTNYELDIKETITLTKPEGFVWAKSKKIPGGTSPSPSTEQSAKKVRKKAENAHT 480
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Db 481 PLLVLYGSNMGTAEGTARDLADIAMSGKGFAPQVATLDSHAGNLPREGAVLIVTASYNHGP 540
QY 541 PDNAKQVFDWLQDASADEVKGVRYSVFCGCGKNWATTYQKVPAFIDETLAAGAENIADR 600
Db 541 PDNAKQVFDWLQDASADEVKGVRYSVFCGCGKNWATTYQKVPAFIDETLAAGAENIADR 600
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QY 661 AFSTNVVASKELQOPGSGARSTRHLEIELPKAEASQEGDHLGVI PRNTEGIVNRVTAREGL 720
Db 661 AFSTNVVASKELQOPGSGARSTRHLEIELPKAEASQEGDHLGVI PRNTEGIVNRVTAREGL 720
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Db 721 DASQIRLEAEKEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 780
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QY 1021 HOVSEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1021 HOVSEADARLWLOOLEEKGRYAKDVWAG 1048
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## RESULT 4

PCT-US02-11954-2

; Sequence 2, Application PC/TUS0211954

; GENERAL INFORMATION:

; APPLICANT: Cirino, Patrick C.

; APPLICANT: Arnold, Frances H.

; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS

; FILE REFERENCE: 4058/2K237-WO0

; CURRENT APPLICATION NUMBER: PCT/US02/11954

; PRIOR FILING DATE: 2002-04-16

; PRIOR APPLICATION NUMBER: 60/284,215

; PRIOR FILING DATE: 2001-04-16

; PRIOR APPLICATION NUMBER: 60/288,636

; PRIOR FILING DATE: 2001-05-03

; PRIOR APPLICATION NUMBER: 60/340,602

; PRIOR FILING DATE: 2001-12-12

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 1049

; TYPE: PRT

; ORGANISM: Bacillus megaterium

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank / P14779  
; DATABASE ENTRY DATE: 1990-04-01  
; RELEVANT RESIDUES: (1)..(1049)  
PCT-US02-11954-2

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Query Match      100.0%; Score 5457; DB 1; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1  TIKEMPQKTFGELKLPILLNTDKPVQALMKIADDELGEIFKFPAGRVTRYLSSQRLIKE 60
DB 2  TIKEMPQKTFGELKLPILLNTDKPVQALMKIADDELGEIFKFPAGRVTRYLSSQRLIKE 61
QY 61 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAMKGYHAMV 120
DB 62 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAMKGYHAMV 121
QY 121 DIAVLQVQKWERLNADAEHIEVPEDMTRLTDLTIGLCGFNYRNFNSFYRDQPHPPITSMVRA 180
DB 122 DIAVLQVQKWERLNADAEHIEVPEDMTRLTDLTIGLCGFNYRNFNSFYRDQPHPPITSMVRA 181
QY 181 LDEAMNKLQANPDDPAYDENKRFQFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG 240
DB 182 LDEAMNKLQANPDDPAYDENKRFQFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG 241
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVQLKAAEEAARVLD 300
DB 242 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVQLKAAEEAARVLD 301
QY 301 PVPYSYQVQKQLKVVGVNLEALRLWTPAFALSIYAKEDTVLGGEYPLEKGDDELVLIPOL 360
DB 302 PVPYSYQVQKQLKVVGVNLEALRLWTPAFALSIYAKEDTVLGGEYPLEKGDDELVLIPOL 361
QY 361 HRDKTWIGDDVEEFRPERFENPNSAIPQHAFKPGNGQACIGQOQFALHEATLVLGMLKH 420
DB 362 HRDKTWIGDDVEEFRPERFENPNSAIPQHAFKPGNGQACIGQOQFALHEATLVLGMLKH 421
QY 421 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKIPGLGIPSPSTEQSAKKVKKKAENAHNT 480
DB 422 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKIPGLGIPSPSTEQSAKKVKKKAENAHNT 481
QY 481 PLLVLVYGSNMGTAEGTARDLADTAMSKGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
DB 482 PLLVLVYGSNMGTAEGTARDLADTAMSKGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 541
QY 541 PDNAKQFVDWLQASADEVKGYRYSVFGCGDKNWTATYOKVPFIDETLAAKGAENIADR 600
DB 542 PDNAKQFVDWLQASADEVKGYRYSVFGCGDKNWTATYOKVPFIDETLAAKGAENIADR 601
QY 601 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAAADPLAKMHG 660
DB 602 GEADASDDFEGTYEWRHMSDVAAYFNLDIENSEDNKSTLSLQFVDSAAADPLAKMHG 661
QY 661 AFSTNVVASKELQOQPSARSTRHELELPKEASYQEGDHLGVIPRNYEGIVNRTARFGL 720
DB 662 AFSTNVVASKELQOQPSARSTRHELELPKEASYQEGDHLGVIPRNYEGIVNRTARFGL 721
QY 721 DASQOIRLEAEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAATVCPPHKVEL 780
DB 722 DASQOIRLEAEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAATVCPPHKVEL 781
QY 781 EALLEKQAYKEQVLAKRLTMELELKY PACEMKFSFIALLPISRPRIYSSISSPRVDEK 840
DB 782 EALLEKQAYKEQVLAKRLTMELELKY PACEMKFSFIALLPISRPRIYSSISSPRVDEK 841
QY 841 QASITVSVYSGEAWSGYGYKGTASNYLAELQEGDTITCFISTPQSEFFLPKDPETPLIM 900
DB 842 QASITVSVYSGEAWSGYGYKGTASNYLAELQEGDTITCFISTPQSEFFLPKDPETPLIM 901
QY 901 VGPCTGVAFPRGFQVARKQKQEGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 960
DB 902 VGPCTGVAFPRGFQVARKQKQEGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 961
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QY 961 HTAFSRMPNQPKTYVQHVMEQDGKKLIELDQGAHFYICGDSQMAPAVEATLMKSYADV 1020
DB 962 HTAFSRMPNQPKTYVQHVMEQDGKKLIELDQGAHFYICGDSQMAPAVEATLMKSYADV 1021
QY 1021 HQVSEADARLWLOOLEEKGRYAKDVWAG 1048
DB 1022 HQVSEADARLWLOOLEEKGRYAKDVWAG 1049

RESULT 5
US-09-791-537-53927
; Sequence 53927, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53927
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
US-09-791-537-53927
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Query Match      100.0%; Score 5457; DB 21; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1  TIKEMPQKTFGELKLPILLNTDKPVQALMKIADDELGEIFKFPAGRVTRYLSSQRLIKE 60
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DB 62 ACDESFRDKNLSQALKFVRDFAGDGLFTSWTHEKNKKAHNILLPSFSQAMKGYHAMV 121
QY 121 DIAVLQVQKWERLNADAEHIEVPEDMTRLTDLTIGLCGFNYRNFNSFYRDQPHPPITSMVRA 180
DB 122 DIAVLQVQKWERLNADAEHIEVPEDMTRLTDLTIGLCGFNYRNFNSFYRDQPHPPITSMVRA 181
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DB 182 LDEAMNKLQANPDDPAYDENKRFQFQEDIKVNDLVDKIIADRKASGEQSDLLTHMLNG 241
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVQLKAAEEAARVLD 300
DB 242 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVQLKAAEEAARVLD 301
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DB 302 PVPYSYQVQKQLKVVGVNLEALRLWTPAFALSIYAKEDTVLGGEYPLEKGDDELVLIPOL 361
QY 361 HRDKTWIGDDVEEFRPERFENPNSAIPQHAFKPGNGQACIGQOQFALHEATLVLGMLKH 420
DB 362 HRDKTWIGDDVEEFRPERFENPNSAIPQHAFKPGNGQACIGQOQFALHEATLVLGMLKH 421
QY 421 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKIPGLGIPSPSTEQSAKKVKKKAENAHNT 480
DB 422 FDFEDHTNYELDIKETLTLPKEGVVYKAKSKIPGLGIPSPSTEQSAKKVKKKAENAHNT 481
QY 481 PLLVLVYGSNMGTAEGTARDLADTAMSKGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 540
DB 482 PLLVLVYGSNMGTAEGTARDLADTAMSKGFAPQVATLDSHAGNLPREGAVLIVTASNGHP 541
QY 541 PDNAKQFVDWLQASADEVKGYRYSVFGCGDKNWTATYOKVPFIDETLAAKGAENIADR 600
DB 542 PDNAKQFVDWLQASADEVKGYRYSVFGCGDKNWTATYOKVPFIDETLAAKGAENIADR 601
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QY 601 GEADASDDFGTGYEWEHWMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 660  
 DB 602 GEADASDDFGTGYEWEHWMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 661  
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 DB 662 AFSTNVVASKELQPGSARSTRHLELPEKASVQEGDHLGVIPRNYEGIVNVRTARFGL 721  
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 DB 722 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781  
 QY 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKFSFIALPSIRPRYISSSPRVDEK 840  
 DB 782 EALLEKQAYKEQVLAKRLTMELEKYPACEMKFSFIALPSIRPRYISSSPRVDEK 841  
 QY 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900  
 DB 842 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 901  
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 DB 902 VGPCTGVAPRFGFVQARKQLKEQGSIGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 961  
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 DB 962 HTAFSRMPNPKTYVQVHVMQDGKLLIQLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021  
 QY 1021 HQVSEADARLWLOOLEEKGRYAKDVWAG 1048  
 DB 1022 HQVSEADARLWLOOLEEKGRYAKDVWAG 1049

RESULT 6

US-10-031-146-9  
 ; Sequence 9, Application US/10031146  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HAUER, Bernhard  
 ; APPLICANT: PLEISS, Juergen  
 ; APPLICANT: SCHWANE, Ulrich  
 ; APPLICANT: SCHMITT, Jutta  
 ; TITLE OF INVENTION: Novel cytochrome p450 monooxygenases and their use for the oxidat  
 ; FILE REFERENCE: 50915  
 ; CURRENT APPLICATION NUMBER: US/10/031,146  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: PCT/EP 00/07253  
 ; PRIOR FILING DATE: 2000-07-27  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: Word Perfect version 6.1  
 ; SEQ ID NO 9  
 ; LENGTH: 1049  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus megaterium  
 US-10-031-146-9

Query Match 100.0%; Score 5457; DB 24; Length 1049;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 2 TIKEMPQKTFGELKNLPILNTDKPVQALMKIADELGEIFKFPAGRVTRYLSSORLIKE 61  
 QY 61 ACDESREDKNLSQALKVPRDFAGDGLFTSWTHEKNKKKAHNLPPSQQAMGYHAMV 120  
 DB 62 ACDESREDKNLSQALKVPRDFAGDGLFTSWTHEKNKKKAHNLPPSQQAMGYHAMV 121  
 QY 121 DIAVOLQVQKWERLNADIEHVEPDMTRTLTDIGLCGFNRYFNFSFYDQPHPTTSVRA 180  
 DB 122 DIAVOLQVQKWERLNADIEHVEPDMTRTLTDIGLCGFNRYFNFSFYDQPHPTTSVRA 181  
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DB 182 LDEAMNKLQRPANPDPPAYDENKQFQEDIKVMDLVDKIIADRRKASGEQSDLLTHMLNG 241  
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 DB 242 KDPETGPDLDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVD 301  
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 QY 361 HRDKTWGDVDEEPRPERFENPSAIPQAFKPFNGORACIGQGFALHEATVLYGMLKH 420  
 DB 362 HRDKTWGDVDEEPRPERFENPSAIPQAFKPFNGORACIGQGFALHEATVLYGMLKH 421  
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 DB 422 FDEEDHNYELDKETLTLKPEGVVKAISKKIPGLGIPSPSTQSKAKYKKAENAHT 481  
 QY 481 PLLVLYGSNMGTAEGTARDLADIAAMSKGFAPOVATLDSHAGNLPREGAVLIVTASYNGHP 540  
 DB 482 PLLVLYGSNMGTAEGTARDLADIAAMSKGFAPOVATLDSHAGNLPREGAVLIVTASYNGHP 541  
 QY 541 PDNAKQFVMDLQASADEVKGVRYSVFCGDKKNWATYQKVPAPIDETLAAGAENIADR 600  
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 DB 602 GEADASDDFGTGYEWEHWMWSVAAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 661  
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 DB 662 AFSTNVVASKELQPGSARSTRHLELPEKASVQEGDHLGVIPRNYEGIVNVRTARFGL 721  
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 DB 722 DASQOIRLEAEEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 781  
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 DB 842 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 901  
 QY 901 VGPCTGVAPRFGFVQARKQLKEQGSIGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 960  
 DB 902 VGPCTGVAPRFGFVQARKQLKEQGSIGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 961  
 QY 961 HTAFSRMPNPKTYVQVHVMQDGKLLIQLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 DB 962 HTAFSRMPNPKTYVQVHVMQDGKLLIQLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021  
 QY 1021 HQVSEADARLWLOOLEEKGRYAKDVWAG 1048  
 DB 1022 HQVSEADARLWLOOLEEKGRYAKDVWAG 1049

RESULT 7

US-10-125-640-2  
 ; Sequence 2, Application US/10125640  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cirino, Patrick C.  
 ; APPLICANT: Arnold, Frances H.  
 ; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS  
 ; FILE REFERENCE: 4058/1K237-US3  
 ; CURRENT APPLICATION NUMBER: US/10/125,640  
 ; CURRENT FILING DATE: 2002-04-16  
 ; PRIOR APPLICATION NUMBER: 60/284,215  
 ; PRIOR FILING DATE: 2001-04-16  
 ; PRIOR APPLICATION NUMBER: 60/288,636

; PRIOR FILING DATE: 2001-05-03  
 ; PRIOR APPLICATION NUMBER: 60/340,602  
 ; PRIOR FILING DATE: 2001-12-12  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 1049  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus megaterium  
 ; PUBLIC INFORMATION:  
 ; DATABASE ACCESSION NUMBER: GenBank / P14779  
 ; DATABASE ENTRY DATE: 1990-04-01  
 ; RELEVANT RESIDUES: (1)..(1049)  
 US-10-125-640-2

Query Match 100.0%; Score 5457; DB 25; Length 1049;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	2	TIKEMPQKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSQRLIKE	61
QY	61	ACDESFRDNLQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	120
DB	62	ACDESFRDNLQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	121
QY	121	DIAVQLQKWERLNADHEIEVPEDMTRLTDLTIGLCGFYRNSFYRDPHPFITSMVRA	180
DB	122	DIAVQLQKWERLNADHEIEVPEDMTRLTDLTIGLCGFYRNSFYRDPHPFITSMVRA	181
QY	181	LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIIADKASGEQSDLLTHMLNG	240
DB	182	LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIIADKASGEQSDLLTHMLNG	241
QY	241	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD	300
DB	242	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD	301
QY	301	PVPSYKQVKQLKVGVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPO	360
DB	302	PVPSYKQVKQLKVGVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPO	361
QY	361	HRDKTIWDDVEEFRPERFENPFAIPQHAFFPGNGQACIGQQFALHEATLVGLMMLKH	420
DB	362	HRDKTIWDDVEEFRPERFENPFAIPQHAFFPGNGQACIGQQFALHEATLVGLMMLKH	421
QY	421	DFEDHTNYELDIKETLTLPKPGFVVKAKSKKIPIGGIPSPSTEQSAKKVKKAEHAHT	480
DB	422	DFEDHTNYELDIKETLTLPKPGFVVKAKSKKIPIGGIPSPSTEQSAKKVKKAEHAHT	481
QY	481	PLLVLYGNNGTAGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIYVTSYNGHP	540
DB	482	PLLVLYGNNGTAGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIYVTSYNGHP	541
QY	541	PONAKQFVWLQOASADEKVGVRYSVFGCGDKNNWATTYOKVPAFIDETLAAGAENIADR	600
DB	542	PONAKQFVWLQOASADEKVGVRYSVFGCGDKNNWATTYOKVPAFIDETLAAGAENIADR	601
QY	601	GEADASDDFEGTYEERHWSQVAAVFNLDIENSEDNKSTLSLOFVDSAAADMPKMHG	660
DB	602	GEADASDDFEGTYEERHWSQVAAVFNLDIENSEDNKSTLSLOFVDSAAADMPKMHG	661
QY	661	AFSTNVVASKELQPGSARSTRHLEIETLPKEASYQEGDHLGVIIPRNYEGIVNRVTA	720
DB	662	AFSTNVVASKELQPGSARSTRHLEIETLPKEASYQEGDHLGVIIPRNYEGIVNRVTA	721
QY	721	DASQIIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPKHKVEL	780
DB	722	DASQIIRLEAEKEKLAHLPLAKTVSVEELQYVELQDPVTRTQLRAMAAKTVCPKHKVEL	781
QY	781	EALLEKQAYKEQVLAKRLTMELEKYPACEMKFEETALLPSIRPRYSSISSPRVDEK	840

DB	782	EALLEKQAYKEQVLAKRLTMELEKYPACEMKFEETALLPSIRPRYSSISSPRVDEK	841
QY	841	QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDITTCFISTPOSEFTLPKDPETPLIM	900
DB	842	QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDITTCFISTPOSEFTLPKDPETPLIM	901
QY	901	VGPGTGVAPFRGFGVQARKQKQGGSLGSAHLYFGCRSPHEDYLYQEELNAQSEGIITL	960
DB	902	VGPGTGVAPFRGFGVQARKQKQGGSLGSAHLYFGCRSPHEDYLYQEELNAQSEGIITL	961
QY	961	HTAFSRMPNQPKTYVQHVMEQDGKLIELLDQGAHFIYICGDSQMAPAVEATLMKSYADV	1020
DB	962	HTAFSRMPNQPKTYVQHVMEQDGKLIELLDQGAHFIYICGDSQMAPAVEATLMKSYADV	1021
QY	1021	HQVSADARLWLOOLEEKGRYAKDYWAG	1048
DB	1022	HQVSADARLWLOOLEEKGRYAKDYWAG	1049

## RESULT 8

US-10-201-213-2  
 ; Sequence 2: Application US/10201213  
 ; GENERAL INFORMATION:  
 ; APPLICANT: California Institute of Technology  
 ; APPLICANT: Farinas, Edgardo  
 ; APPLICANT: Glieder, Anton  
 ; APPLICANT: Arnold, Frances  
 ; APPLICANT: Schwanberg, Ulrich  
 ; TITLE OF INVENTION: IMPROVED CYTOCHROME P450 OXYGENASES  
 ; FILE REFERENCE: 3369/1K238-US2  
 ; CURRENT APPLICATION NUMBER: US/10/201,213  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: US 60/306,766  
 ; PRIOR FILING DATE: 2001-07-20  
 ; PRIOR APPLICATION NUMBER: US 60/308,429  
 ; PRIOR FILING DATE: 2001-07-27  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 1049  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus megaterium  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: GenBank / P14779  
 ; DATABASE ENTRY DATE: 1990-04-01  
 ; RELEVANT RESIDUES: (1)..(1049)  
 US-10-201-213-2

Query Match 100.0%; Score 5457; DB 26; Length 1049;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TIKEMPQKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSQRLIKE	60
DB	2	TIKEMPQKTFGELKNLPLNTDKPVQALMKIADDELGEIFKFEAPGRVTRYLSSQRLIKE	61
QY	61	ACDESFRDNLQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	120
DB	62	ACDESFRDNLQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMKGYHAMV	121
QY	121	DIAVQLQKWERLNADHEIEVPEDMTRLTDLTIGLCGFYRNSFYRDPHPFITSMVRA	180
DB	122	DIAVQLQKWERLNADHEIEVPEDMTRLTDLTIGLCGFYRNSFYRDPHPFITSMVRA	181
QY	181	LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIIADKASGEQSDLLTHMLNG	240
DB	182	LDEAMNKLQANPDDPAYDENKRFQEDIKVMNDLVDKIIADKASGEQSDLLTHMLNG	241
QY	241	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD	300
DB	242	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLD	301
QY	301	PVPSYKQVKQLKVGVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIPO	360

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Db 302 PVPYKQVQKQKLVYGVMLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIQOL 361
Qy 361 HRDXTINGDDVEEPRPERFENPSAIPQHAFFPGNGQACIGQOFALHEATLVLGMLKH 420
Db 362 HRDXTINGDDVEEPRPERFENPSAIPQHAFFPGNGQACIGQOFALHEATLVLGMLKH 421
Qy 421 FDFEDHNYELDIKETITLTKPEGFVVKAKSKIPGLGIPSPSTQSAKKVKKKAENAHNT 480
Db 422 FDFEDHNYELDIKETITLTKPEGFVVKAKSKIPGLGIPSPSTQSAKKVKKKAENAHNT 481
Qy 481 PLLVLYGSMGTAGTARDLADIAWSKGAFQVATLDSHAGNLPREGAVLIVTASYNGHP 540
Db 482 PLLVLYGSMGTAGTARDLADIAWSKGAFQVATLDSHAGNLPREGAVLIVTASYNGHP 541
Qy 541 PDNAKQFVMDLQASADEVKGVYVFCGCGDKNATYQKPAFTDETTLAAKGAENIADR 600
Db 542 PDNAKQFVMDLQASADEVKGVYVFCGCGDKNATYQKPAFTDETTLAAKGAENIADR 601
Qy 601 GEADASDDFEGTYEWEHMHMSDVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 660
Db 602 GEADASDDFEGTYEWEHMHMSDVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 661
Qy 661 AFSTNVVASKELQOPGSGARSSTRHLEIELPKEAQOEGDHLGVIIPRNYEGIVNRVTARFGL 720
Db 662 AFSTNVVASKELQOPGSGARSSTRHLEIELPKEAQOEGDHLGVIIPRNYEGIVNRVTARFGL 721
Qy 721 DASQOIRLEAEKEELAHPLAKTVSVEELQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 780
Db 722 DASQOIRLEAEKEELAHPLAKTVSVEELQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 781
Qy 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKSEFIALPSPRPRYSISSSPRVDEK 840
Db 782 EALLEKQAYKEQVLAKRLTMELEKYPACEMKSEFIALPSPRPRYSISSSPRVDEK 841
Qy 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTQPOSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTQPOSEFTLPKDPETPLIM 901
Qy 901 VPGTGVAPFRGFGVQARKQLKEQGSLSGEAHLFGCRSPHEDYLYQEELENAQSEGIITL 960
Db 902 VPGTGVAPFRGFGVQARKQLKEQGSLSGEAHLFGCRSPHEDYLYQEELENAQSEGIITL 961
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## RESULT 9

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US-09-856-339A-21
; Sequence 21, Application US/09856339A
; GENERAL INFORMATION:
; APPLICANT: Wong, Luet
; APPLICANT: Bell, Stephen
; APPLICANT: Carmichael, Angus
; TITLE OF INVENTION: PROCESS FOR OXIDISING TERPENES
; FILE REFERENCE: HO-P021960S0 (10104571)
; CURRENT APPLICATION NUMBER: US/09/856.339A
; CURRENT FILING DATE: 2001-05-18
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: GB 9825421.2
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Bacillus megaterium
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; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (1)..(1049)
; OTHER INFORMATION: Coding sequence
US-09-856-339A-21

Query Match 99.9%; Score 5449; DB 22; Length 1049;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TIKEMPOKPTGELKKNLPLLNTDKPVQALMKIADLGEIFKFEAPGRVTRYLSSORLIKE 60
Db 2 TIKEMPOKPTGELKKNLPLLNTDKPVQALMKIADLGEIFKFEAPGRVTRYLSSORLIKE 61
Qy 61 ACDSERFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNLLPSPFSQQAAMKGYHAMV 120
Db 62 ACDSERFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNLLPSPFSQQAAMKGYHAMV 121
Qy 121 DIAVOLVQKWERLNADHEIEVPEDWTRTLTDTIGLCGFNYRNFNSFYRDPHPFITSMVRA 180
Db 122 DIAVOLVQKWERLNADHEIEVPEDWTRTLTDTIGLCGFNYRNFNSFYRDPHPFITSMVRA 181
Qy 181 LDEAMNKLQRANPDPPAYDENKROFQEDIKYMNDLVDKIIADRKASGQSDLLTHMLNG 240
Db 182 LDEAMNKLQRANPDPPAYDENKROFQEDIKYMNDLVDKIIADRKASGQSDLLTHMLNG 241
Qy 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLVD 300
Db 242 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLVD 301
Qy 301 PVPYKQVQKQKLVYGVMLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIQOL 360
Db 302 PVPYKQVQKQKLVYGVMLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLIQOL 361
Qy 361 HRDXTINGDDVEEPRPERFENPSAIPQHAFFPGNGQACIGQOFALHEATLVLGMLKH 420
Db 362 HRDXTINGDDVEEPRPERFENPSAIPQHAFFPGNGQACIGQOFALHEATLVLGMLKH 421
Qy 421 FDFEDHNYELDIKETITLTKPEGFVVKAKSKIPGLGIPSPSTQSAKKVKKKAENAHNT 480
Db 422 FDFEDHNYELDIKETITLTKPEGFVVKAKSKIPGLGIPSPSTQSAKKVKKKAENAHNT 481
Qy 481 PLLVLYGSMGTAGTARDLADIAWSKGAFQVATLDSHAGNLPREGAVLIVTASYNGHP 540
Db 482 PLLVLYGSMGTAGTARDLADIAWSKGAFQVATLDSHAGNLPREGAVLIVTASYNGHP 541
Qy 541 PDNAKQFVMDLQASADEVKGVYVFCGCGDKNATYQKPAFTDETTLAAKGAENIADR 600
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Qy 601 GEADASDDFEGTYEWEHMHMSDVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 660
Db 602 GEADASDDFEGTYEWEHMHMSDVAAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 661
Qy 661 AFSTNVVASKELQOPGSGARSSTRHLEIELPKEAQOEGDHLGVIIPRNYEGIVNRVTARFGL 720
Db 662 AFSTNVVASKELQOPGSGARSSTRHLEIELPKEAQOEGDHLGVIIPRNYEGIVNRVTARFGL 721
Qy 721 DASQOIRLEAEKEELAHPLAKTVSVEELQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 780
Db 722 DASQOIRLEAEKEELAHPLAKTVSVEELQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 781
Qy 781 EALLEKQAYKEQVLAKRLTMELEKYPACEMKSEFIALPSPRPRYSISSSPRVDEK 840
Db 782 EALLEKQAYKEQVLAKRLTMELEKYPACEMKSEFIALPSPRPRYSISSSPRVDEK 841
Qy 841 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTQPOSEFTLPKDPETPLIM 900
Db 842 QASITVSVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTQPOSEFTLPKDPETPLIM 901
Qy 901 VPGTGVAPFRGFGVQARKQLKEQGSLSGEAHLFGCRSPHEDYLYQEELENAQSEGIITL 960
Db 902 VPGTGVAPFRGFGVQARKQLKEQGSLSGEAHLFGCRSPHEDYLYQEELENAQSEGIITL 961
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QY 961 HTAFSRMPNPKTYVHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
Db 962 HTAFSRMPNPKTYVHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021  
QY 1021 HOVSEADARLWLOOLEEKGRYAKDVWAG 1048  
Db 1022 HOVSEADARLWLOOLEEKGRYAKDVWAG 1049  
RESULT 10  
US-10-018-730A-4  
; Sequence 4, Application US/10018730A  
; GENERAL INFORMATION:  
; APPLICANT: Luet, Wong  
; APPLICANT: Jonathan, Jones  
; TITLE OF INVENTION: PROCESS FOR OXIDISING AROMATIC COMPOUNDS  
; FILE REFERENCE: P02353051 / 10112404 / N.76277B  
; CURRENT APPLICATION NUMBER: US/10/018,730A  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: GB 9914373.7  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: PCT/GB00/02379  
; PRIOR FILING DATE: 2000-06-19  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 1049  
; TYPE: PRT  
; ORGANISM: Bacillus megaterium  
US-10-018-730A-4  
Query Match 99.9%; Score 5449; DB 24; Length 1049;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TIKEMPOPKTGELKNPLINTDKPVQALMKIADELGEIFKFPAGRVTRYLSSORLIKE 60  
Db 2 TIKEMPOPKTGELKNPLINTDKPVQALMKIADELGEIFKFPAGRVTRYLSSORLIKE 61  
QY 61 ACDESFRDNLSALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQAMKGYHAMV 120  
Db 62 ACDESFRDNLSALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQAMKGYHAMV 121  
QY 121 DIAVOLQVQWERLNADHEIEVDPEDTRLTDLTGLCGFNFRFNSFYRDOPHPITSMVRA 180  
Db 122 DIAVOLQVQWERLNADHEIEVDPEDTRLTDLTGLCGFNFRFNSFYRDOPHPITSMVRA 181  
QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVMDLVDKIIADRKASGEQSDLLTHMLNG 240  
Db 182 LDEAMNKLQANPDDPAYDENKRFQEDIKVMDLVDKIIADRKASGEQSDLLTHMLNG 241  
QY 241 KDPETGEPLDDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHYLQAAEAAARVLD 300  
Db 242 KDPETGEPLDDENIRYQIITFLTAGHETTSGLLSFALYFLVKNPHYLQAAEAAARVLD 301  
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QY 361 HRDKTITWDDVEFRERENPNSAIPQHAFFKPGNGQRACIGQGFALHEATLVGLMMLKH 420  
Db 362 HRDKTITWDDVEFRERENPNSAIPQHAFFKPGNGQRACIGQGFALHEATLVGLMMLKH 421  
QY 421 FDFEDHTNYELDKETLTKPEGFVVKAKSKKIPLGIPSPTEQSAKKVKAENAHNT 480  
Db 422 FDFEDHTNYELDKETLTKPEGFVVKAKSKKIPLGIPSPTEQSAKKVKAENAHNT 481  
QY 481 PLLVLVYGSNMGTAEGTARDLADIAKSGAPQVATLDHAGNLPREGAVLIVTASNGHP 540  
Db 482 PLLVLVYGSNMGTAEGTARDLADIAKSGAPQVATLDHAGNLPREGAVLIVTASNGHP 541  
QY 541 PDNAKFVWDLQASADEVKGVRYSVFGCGDKNWTYQKVPAFIDETLAAGAENIADR 600

Db 542 PDNAKFVWDLQASADEVKGVRYSVFGCGDKNWTYQKVPAFIDETLAAGAENIADR 601  
QY 601 GEADASDDFEGTYEERHWNWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 660  
Db 602 GEADASDDFEGTYEERHWNWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADPLAKMHG 661  
QY 661 AFSTNVVASKELQOQPGSARSSTRHLEIETELPKEASYQBGDHLGVIPRNVETGIVNRVTAARFGL 720  
Db 662 AFSTNVVASKELQOQPGSARSSTRHLEIETELPKEASYQBGDHLGVIPRNVETGIVNRVTAARFGL 721  
QY 721 DASQQIRLEAEAEKLAHLPLAKTVSVEELLQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 780  
Db 722 DASQQIRLEAEAEKLAHLPLAKTVSVEELLQYVELQDPVTRTOLRAMAAKTVCPPHKVEL 781  
QY 781 EALLEKQAYKEQVLAKRLTLMLELLEKYPACEMKSEFIALLPISIRPRYSISSPRVDEK 840  
Db 782 EALLEKQAYKEQVLAKRLTLMLELLEKYPACEMKSEFIALLPISIRPRYSISSPRVDEK 841  
QY 841 QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDITICFISTPQSEFTLPKDPETPLIM 900  
Db 842 QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDITICFISTPQSEFTLPKDPETPLIM 901  
QY 901 VGPGTGVADPFRGVQARKOLKEQOQSLGEAHLFYGCRSPHEDYLYOELENAQSEGIITL 960  
Db 902 VGPGTGVADPFRGVQARKOLKEQOQSLGEAHLFYGCRSPHEDYLYOELENAQSEGIITL 961  
QY 961 HTAFSRMPNPKTYVHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
Db 962 HTAFSRMPNPKTYVHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021  
QY 1021 HOVSEADARLWLOOLEEKGRYAKDVWAG 1048  
Db 1022 HOVSEADARLWLOOLEEKGRYAKDVWAG 1049  
RESULT 11  
PCT-US02-11954-6  
; Sequence 6, Application PC/TUS0211954  
; GENERAL INFORMATION:  
; APPLICANT: Cirino, Patrick C.  
; APPLICANT: Arnold, Frances H.  
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS  
; FILE REFERENCE: 4058/2K237-W00  
; CURRENT APPLICATION NUMBER: PCT/US02/11954  
; CURRENT FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: 60/284,215  
; PRIOR FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 60/288,636  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: 60/340,602  
; PRIOR FILING DATE: 2001-12-12  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 6  
; LENGTH: 1061  
; TYPE: PRT  
; ORGANISM: Bacillus subtilis  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank / 008394  
; DATABASE ENTRY DATE: 2001-10-16  
; RELEVANT RESIDUES: (1)..(1061)  
PCT-US02-11954-6  
Query Match 60.7%; Score 3314; DB 1; Length 1061;  
Best Local Similarity 59.5%; Pred. No. 1e-287;  
Matches 628; Conservative 156; Mismatches 259; Indels 12; Gaps 6;  
QY 5 MPQKTFGELKNPLINTDKPVQALMKIADELGEIFKFPAGRVTRYLSSORLIKEACDE 64  
Db 7 IQPQTFGELGNLPLIDKDKPTLSLKLAEQGPFIQHTPACTIVVSGHELKVECD 66  
QY 65 SRFDKNLSALKFVRDFAGDGLFTSWTHEKNWKAHNILLPFSQAMKGYHAMVADI 124



Db 67 ERFDKSTEGALEKVRAPSGDGLFTSWTHPEWNRKAHNLMPFTSQRAMKDYHEKMDVIAV 126  
Qy 125 QLVQKWERLNADEHIEVPEDMTLTLDTIGLCGFNYRFSYRDPHPFTITSMVRALDEA 184  
Db 127 QLVQKWARLNPNEAVDPGDMTRTLDTIGLCGFNYRFSYRDPHPFTITSMVRALDEA 186  
Qy 185 MNKLQANPDPPADYENKROFQEDIKVMNDLVKIIADRAKASGQSD-DLLTHMLNGKDP 243  
Db 187 MHQMRDLVDQKLMVTRKQFRYDIQTMFSILVDSIIAERRANGDQDEKDLARMLNVDP 246  
Qy 244 ETGPELDDENIRQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLVDVP 303  
Db 247 ETGKLDENIRQIITFLIAGHETTSGLLSFATYFLKHPDKLKAYEEDVRLTDAAP 306  
Qy 304 SYKQVKOLKYGVMLNEALRLWPTAPAFSLYAKEDTVLGGYPLEKGDGLMVLIPOLHRD 363  
Db 307 TYKQVLELTYIRMLNESLRLWPTAPAFSLYKPEDTVIGGKFTTNDRIISVLIPOLHRD 366  
Qy 364 KTIWGDDEVEEPRPERFENPSAIPQAFKPGNGQACIGQOQFALHEATLVLMKMLKHDF 423  
Db 367 RDWANGKDAEERPERFEHQDQVPHAYKPGNGQACIGQOQFALHEATLVLMKMLKYFTL 426  
Qy 424 EDHTNYELDKETITLTKPEGFVVKAKSKKIPLGIPSPSTEQSA---KVRKKAENA--- 477  
Db 427 IDHENYELDIKQTLTKPGDFHISVQSRHQEAIHADVQAAEKAAPDQKTEAKGASVI 486  
Qy 478 --HNTPLLVLYGSNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTAS 535  
Db 487 GLNRRPLLVLYGSDTGAEGVARELADTASLHGVRTKTAPLNDRIKGLPKKEGAVVIVTSS 546  
Qy 536 YNGHPPDNAQOFVDMQLQASADEKVGVRYSVFGCGDKNWAITYQKVPFIDETLAAGAE 595  
Db 547 YNGKPPNAGQFVQMLQEIKEPGELEGVHYAVFGCGDNWASTYQVVPREFIDQLAERGAT 606  
Qy 596 NIADRGADADDDFEGTYEWEHREHMSDVAAYFNLDI-ENSEDNKSTLSLOFVDSAADMP 654  
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Qy 655 LAKMHGAFSTWVAVASKELQOPGASRSTRHLIELPKAEASQYEGDHLGVIPRNYGVNVR 714  
Db 666 LARSYEASHASIAENRELQASDSRSTRHIFIALPPDVEYQEGDHLGVLPKNSQTNVRI 726  
Qy 715 TARGGLDASQIRLEAEBEKLALPLAKTVSVEBLLQY-VELQDPVTRTOLRAAAKTV 773  
Db 727 LHREGLKGTQVTLASGRSAGHLPLGRPVSLHDLLSYSVEVQEAATRAQIRELASFTVC 786  
Qy 774 PPHKVEALELLEKQAYKEOVLAKRLTWLELLEKYPACEMKFEFIALPSTRPYXSTSS 833  
Db 787 PPHRRELELSAEGVYQEQILKRIKRIKRIKRIKRIKRIKRIKRIKRIKRIKRIKRIKRI 846  
Qy 834 SPRYDEKQASITVSWSGEAWSGYKYGKIASNYLAELQEGDTITCFISTPQSEFTLPKD 893  
Db 847 SPRYNPQASITVGVVGRPAWNGRGEYRGVANSNDLAERQAGDDVVMIRPESRFPQPKD 906  
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Qy 954 SEGIITHTAFSRPNPQKTYVQHVNEQDQKLLLELDQGAHFICGDSGQMAFAVATL 1013  
Db 966 KDGITVHTAFSRGEGPKTYVQVHLMADQADTLISILDRGRLYVCGDSGSKMAPDVEAAL 1025  
Qy 1014 MKSYADHVQVSEADARLQOOLEEKGRYAKDVWAG 1048  
Db 1026 QKAYQAVHGTGEQEAQNLRLHQDTGMTAKDVWAG 1060

RESULT 12  
PCT-US02-11954-7  
; Sequence 7, Application PC/TUS0211954  
; GENERAL INFORMATION:  
; APPLICANT: Cirino, Patrick C.

; APPLICANT: Arnold, Frances H.  
; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS  
; FILE REFERENCE: 4058/2K37-WO  
; CURRENT APPLICATION NUMBER: PCT/US02/11954  
; CURRENT FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: 60/284,215  
; PRIOR FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 60/288,636  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: 60/340,602  
; PRIOR FILING DATE: 2001-12-12  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 1061  
; TYPE: PRT  
; ORGANISM: Bacillus subtilis  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank / D69799  
; DATABASE ENTRY DATE: 2000-07-28  
; RELEVANT RESIDUES: (1)..(1061)  
PCT-US02-11954-7

Query Match 60.7%; Score 3314; DB 1; Length 1061;  
Best Local Similarity 59.5%; Pred. No. 1e-287;  
Matches 628; Conservative 156; Mismatches 259; Indels 12; Gaps 6;

Qy 5 MPQPKTGEKLNKLLANTDKPQALMKIADLGEIKFEKFAEAPGRTVRLYSSQRLIKEACDE 64  
Db 7 IPQKTFGPGNLPLIDKDKPTLSLIKAEQGGPIQIHTPAGTIIVVSGHELKVEUCDE 66  
Qy 65 SRFQKNSQALKFYRDFAGDGLFTSWTHKKNKKAHNLILPFSQQAQMGVHAMVMDIAV 124  
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Qy 125 QLVQKWERLNADEHIEVPEDMTLTLDTIGLCGFNYRFSYRDPHPFTITSMVRALDEA 184  
Db 127 QLVQKWARLNPNEAVDPGDMTRTLDTIGLCGFNYRFSYRDPHPFTITSMVRALDEA 186  
Qy 185 MNKLQANPDPPADYENKROFQEDIKVMNDLVKIIADRAKASGQSD-DLLTHMLNGKDP 243  
Db 187 MHQMRDLVDQKLMVTRKQFRYDIQTMFSILVDSIIAERRANGDQDEKDLARMLNVDP 246  
Qy 244 ETGPELDDENIRQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLVDVP 303  
Db 247 ETGKLDENIRQIITFLIAGHETTSGLLSFATYFLKHPDKLKAYEEDVRLTDAAP 306  
Qy 304 SYKQVKOLKYGVMLNEALRLWPTAPAFSLYAKEDTVLGGYPLEKGDGLMVLIPOLHRD 363  
Db 307 TYKQVLELTYIRMLNESLRLWPTAPAFSLYKPEDTVIGGKFTTNDRIISVLIPOLHRD 366  
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Qy 424 EDHTNYELDKETITLTKPEGFVVKAKSKKIPLGIPSPSTEQSA---KVRKKAENA--- 477  
Db 427 IDHENYELDIKQTLTKPGDFHISVQSRHQEAIHADVQAAEKAAPDQKTEAKGASVI 486  
Qy 478 --HNTPLLVLYGSNMGTAEGTARDLADIAKSGFAPQVATLDSHAGNLPREGAVLIVTAS 535  
Db 487 GLNRRPLLVLYGSDTGAEGVARELADTASLHGVRTKTAPLNDRIKGLPKKEGAVVIVTSS 546  
Qy 536 YNGHPPDNAQOFVDMQLQASADEKVGVRYSVFGCGDKNWAITYQKVPFIDETLAAGAE 595  
Db 547 YNGKPPNAGQFVQMLQEIKEPGELEGVHYAVFGCGDNWASTYQVVPREFIDQLAERGAT 606  
Qy 596 NIADRGADADDDFEGTYEWEHREHMSDVAAYFNLDI-ENSEDNKSTLSLOFVDSAADMP 654  
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Qy 655 LAKMHGAFSTWVAVASKELQOPGASRSTRHLIELPKAEASQYEGDHLGVIPRNYGVNVR 714  
Db 666 LARSYEASHASIAENRELQASDSRSTRHIFIALPPDVEYQEGDHLGVLPKNSQTNVRI 726



; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: GenBank / O08394  
 ; DATABASE ENTRY DATE: 2001-10-16  
 ; RELEVANT RESIDUES: (1)..(1061)  
 US-10-125-640-6

Qy	5	MPQKTFGELKNPLNLTDPVQALMKIADLGEIFKEAPGRVTRYLSSORLIKEACDE	64
Db	7	IPQKTFGLNGLNLDKDKPTLSLIKLAEEQGFQIHTPAGTIVVSGHELKVCDE	66
Qy	65	SRFDKNSLQALKFVRDAGDGLFTSWTHKNNKKAHNLPSFSQOAMKGVHAMVVDIAY	124
Db	67	ERFDKSIKALKEKVAESGDLFTSWTHKNNKKAHNLPSFSQOAMKGVHAMVVDIAY	126
Qy	125	QLVOKWRLNADEHIEVPEDMTLTDITGLCGFNRYFNFSYRDPQPHFTTSMVRALDEA	184
Db	127	QLIQKWARLNPNNEAVDPGDMTRLTDTIGLCGFNRYFNFSYRDPQPHFTTSMVRALDEA	186
Qy	185	MNKLQANPPDPAVDENKRFQEDIKVMNDLVDKIIADKASGEQSD-DLLTHMLNGKDP	243
Db	187	MHQMRLDQVKLMVTRKQFRYDIQTMFSLVDSIIAERRANGDQDEKDLARMLNVEDP	246
Qy	244	ETGKPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVDVPP	303
Db	247	ETGKPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVDVPP	306
Qy	304	SYKOVKQKLYGVVGNLNEALRWPTAPASLYAKEDTVLGGYPLEKGDLMVLIPQLHRD	363
Db	307	TYKQVLELYTIRMLNESLRLWPTAPASLYAKEDTVLGGYPLEKGDLMVLIPQLHRD	366
Qy	364	KTINGDDVEEPRPERFENPSAIPQAFKPGNGORACIGQOQFALHEATLVGLMKLHFD	423
Db	367	RDANGKDAEPRPERFENPSAIPQAFKPGNGORACIGQOQFALHEATLVGLMKLHFD	426
Qy	424	EDHTNYELDKETITLTPKGFVVKAKSKKIPGLGIPSPSTQSA---KKVRKKAENA---	477
Db	427	IDHENYELDKETITLTPKGFVVKAKSKKIPGLGIPSPSTQSA---KKVRKKAENA---	486

Qy	954	SEGIITLHTAFSRMPNPKTYVQVHMEQDGKKLIELLDQGAHFYICGDSQMAPAVEATL	1013
Db	966	KDGIIVTHTAFSRKEGPKTYVQVHMEQDGKKLIELLDQGAHFYICGDSQMAPAVEATL	1025
Qy	1014	MKSYADYHVSADARLWLQLEEKRYAKDVMWAG	1048
Db	1026	QKAYQAVHGTGEQEAQNWLRLHLDQTMGYAKDVMWAG	1060

RESULT 15  
 US-10-125-640-7  
 ; Sequence 7, Application US/10125640  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cirino, Patrick C.  
 ; APPLICANT: Arnold, Frances H.  
 ; TITLE OF INVENTION: PROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS  
 ; FILE REFERENCE: 4058/1K237-US3  
 ; CURRENT APPLICATION NUMBER: US/10/125,640  
 ; CURRENT FILING DATE: 2002-04-16  
 ; PRIOR APPLICATION NUMBER: 60/284,215  
 ; PRIOR FILING DATE: 2001-04-16  
 ; PRIOR APPLICATION NUMBER: 60/288,636  
 ; PRIOR FILING DATE: 2001-05-03  
 ; PRIOR APPLICATION NUMBER: 60/340,602  
 ; PRIOR FILING DATE: 2001-12-12  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 1061  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus subtilis  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: GenBank / D69799  
 ; DATABASE ENTRY DATE: 2000-07-28  
 ; RELEVANT RESIDUES: (1)..(1061)  
 US-10-125-640-7

Query Match	60.7%	Score 3314;	DB 25;	Length 1061;
Best Local Similarity	59.5%	Pred. No. 1e-287;		
Matches 628;	Conservative 156;	Mismatches 259;	Indels 12;	Gaps 6;

Qy	5	MPQKTFGELKNPLNLTDPVQALMKIADLGEIFKEAPGRVTRYLSSORLIKEACDE	64
Db	7	IPQKTFGLNGLNLDKDKPTLSLIKLAEEQGFQIHTPAGTIVVSGHELKVCDE	66
Qy	65	SRFDKNSLQALKFVRDAGDGLFTSWTHKNNKKAHNLPSFSQOAMKGVHAMVVDIAY	124
Db	67	ERFDKSIKALKEKVAESGDLFTSWTHKNNKKAHNLPSFSQOAMKGVHAMVVDIAY	126
Qy	125	QLVOKWRLNADEHIEVPEDMTLTDITGLCGFNRYFNFSYRDPQPHFTTSMVRALDEA	184
Db	127	QLIQKWARLNPNNEAVDPGDMTRLTDTIGLCGFNRYFNFSYRDPQPHFTTSMVRALDEA	186
Qy	185	MNKLQANPPDPAVDENKRFQEDIKVMNDLVDKIIADKASGEQSD-DLLTHMLNGKDP	243
Db	187	MHQMRLDQVKLMVTRKQFRYDIQTMFSLVDSIIAERRANGDQDEKDLARMLNVEDP	246
Qy	244	ETGKPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVDVPP	303
Db	247	ETGKPLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAARVLVDVPP	306
Qy	304	SYKOVKQKLYGVVGNLNEALRWPTAPASLYAKEDTVLGGYPLEKGDLMVLIPQLHRD	363
Db	307	TYKQVLELYTIRMLNESLRLWPTAPASLYAKEDTVLGGYPLEKGDLMVLIPQLHRD	366
Qy	364	KTINGDDVEEPRPERFENPSAIPQAFKPGNGORACIGQOQFALHEATLVGLMKLHFD	423
Db	367	RDANGKDAEPRPERFENPSAIPQAFKPGNGORACIGQOQFALHEATLVGLMKLHFD	426
Qy	424	EDHTNYELDKETITLTPKGFVVKAKSKKIPGLGIPSPSTQSA---KKVRKKAENA---	477
Db	427	IDHENYELDKETITLTPKGFVVKAKSKKIPGLGIPSPSTQSA---KKVRKKAENA---	486



Result No.	Score	Match	Length	DB	ID	Description
1	2420.5	44.4	1077	6	US-10-214-446-24	Sequence 24, Appl
2	1945.5	35.7	1073	6	US-10-156-761-8117	Sequence 8117, Ap
3	953.5	17.5	504	6	US-10-156-761-14954	Sequence 14954, A
4	777.5	14.2	677	6	US-10-219-051B-11638	Sequence 11638, A
5	777.5	14.2	677	6	US-10-219-051B-12755	Sequence 12755, A
6	769.14	14.1	682	6	US-10-148-907A-23	Sequence 23, Appl
7	767.14	14.1	676	6	US-10-219-051B-12757	Sequence 12757, A
8	767.14	14.1	677	7	US-60-440-068-572	Sequence 572, App
9	728.5	13.3	689	6	US-10-424-599-187294	Sequence 187294, A
10	712.5	13.1	719	6	US-10-425-114-70174	Sequence 70174, A
11	710.13	13.0	691	6	US-10-424-599-191313	Sequence 191313, A
12	705.5	12.9	588	6	US-10-188-523B-14	Sequence 14, Appl
13	705.5	12.9	588	6	US-10-188-523C-14	Sequence 14, Appl
14	688	12.6	708	6	US-10-424-599-177338	Sequence 177338, A
15	678	12.4	1429	5	US-09-661-258-2	Sequence 2, Appl
16	675	12.4	1199	7	US-60-452-680-23982	Sequence 23982, A
17	675	12.4	1199	7	US-60-453-135-14960	Sequence 14960, A
18	675	12.4	1199	7	US-60-453-050-14960	Sequence 14960, A
19	675	12.4	1199	7	US-60-453-444-8116	Sequence 8116, Ap
20	675	12.4	1199	7	US-60-465-241-8116	Sequence 8116, Ap
21	675	12.4	1434	5	US-09-661-258-1	Sequence 1, Appl
22	665.5	12.2	1144	5	US-09-751-708A-124	Sequence 124, App
23	665.5	12.2	1144	5	US-09-661-258-5	Sequence 5, Appl
24	665	12.2	1153	5	US-09-661-258-4	Sequence 4, Appl
25	661	12.1	1114	5	US-09-724-676-86297	Sequence 86297, A
26	661	12.1	1114	5	US-09-724-676A-86297	Sequence 86297, A



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Db      883 DGRYRCKGSSYIAGLESGDVFGYVRVPSTFPAPPADPATPLLIGTGIAPLGRFLEE 942
      |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.|
QY      917 RKQLEKQCGSLGSAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAFSRMPNQPKTYVQ 976
      |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.|
Db      943 RAHQHAGHTQVGLSVQFVGCRRHPEHDYFYFQEQMDWEQAGIAQVHTAFSAVTCGHPARFVQ 1002
      |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.|
QY      977 HVMEQDGKKLIELLDGAGHIFYCGDGSQMAPAVEATLMKSYADVHVQSEADARLTLQOLE 1036
      |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.|
Db      1003 DAIVGAADTVQWQAIQDGAIVYVCGDGRMAPAVREALAATYRKHTGSDDEAAQQLAQL 1062
      |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.|
QY      1037 EKGRYAKDYWA 1047
      |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.|
Db      1063 ADERYQDWF 1073
      |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.| |.:.|

RESULT 3
US-10-156-761-14954
; Sequence 14954, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14954
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14954

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QY   410 ATVLGMLKHFDHNTVELDIKFTLTKPGFVVVAKSKKIPLGGIPSPSTESA 467
      IIIII::: : I : III III : : I : I :
Db    436 ATVLGLLLLRYELRAEPGYRLRVAERLTLMPEGLRLDRRPAVEDVPANPEVSS 493

RESULT 4
US-10-219-051B-11638
; Sequence 11638, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 11638
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / P00388
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-11638

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[illegible]





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QY 921 KEQOSLGEAHLFGCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPRTYYQHVH 979
Db 555 RQOGKEVETLLYGCRRAAEDYLYREELAGFKDGLTSLQNLNFAVSREQAQ-KVYVQHLL 613
QY 980 EQDGKLIELDDQ-GAHFYICGDSQMAPAVEATLMKSYADVHOVSADARLWLQLEEK 1038
Db 614 RRKEHLRLWLIHEGGAHYIYCGDARNMARDVQNTFYDVAELGAMEHAQAQVYVVKILMTK 673
QY 1039 GRYAKDWA 1047
Db 674 GRYSLDWS 682

RESULT 7
US-10-219-051B-12757
; Sequence 12757, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 12757
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / BAB18572
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-12757

Query Match 14.1%; Score 767; DB 6; Length 676;
Best Local Similarity 32.4%; Pred. No. 1.3e-57;
Matches 211; Conservative 113; Mismatches 264; Indels 64; Gaps 23;

QY 444 FVYKAKSKIP----LGGIPSPSTEQS-AKKVRKAENAHNTPLLVLYGSMGTAEGR 498
Db 41 FLFRKKKEEVPETFKIOTLTSSVRESSEFVEKMKKTGRN-----IIVYGSQTGAEEFAN 95
QY 499 DLADIAKSGFAQVATLDSH----AGNLPREGAVLIV--TASY-NGHPPDNKQFVDWL 551
Db 96 RLSKDAHRYGMRGMSADPEEYDLADLSSLPEDNALVYFCMATYEGEDPTDNAQDFYDWL 155
QY 552 DQASADRVKGVYRVSFCGCKGNWATTYQKVP---FIDETLAAGAENIADRGADASDD 608
Db 156 QETDVD--LSGVKFAVGLGNK-----TYEHFNAMGKYVDKRLQELGAORIFELGLGDDGN 210
QY 609 FEETYEWRHMSDVAAYFNLDIENSEDNKSTLSQF---VDSA-----ADMPLAKMH-- 659
Db 211 LEEDFITWRQFPAVCEHFGVEATGESSIRQYELVVHTDIDAAYVMGEMGLKSYEN 270
QY 660 -----GAFSTNVVASKELQOPGSASTRHLEIEL-PKEASYQEGDHLGVIPRNYEGI 710
Db 271 QKPPFDKPNFLAAVTNNRKLQ--GTERHLMHLELDISDSKIRYESGDHVAVYPANDSAL 329
QY 711 VNRVTARFG--LDASQOIRLEAEEKLAHLPLAKTVSVEELLQYVELQDPVTRTOLRAMA 768
Db 330 VNOLGKTLGADLVVMSNLNDESNKKHPFPCPTSYRTALTYYLDTNP-PRTNVLYEL 398
QY 769 AKTVCPHPKVELEALLE-----KQAYKEQVLAKRLTLMLELLEKYPACEMKSEFIALLP 822
Db 389 AQVASEPSEGLRKKMASSGEGKELYLSWVVEARRHILAILQDCPLRPPIHLCCELLP 448
QY 823 SIRPRYISISSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYL-AELQEGDT----- 876
```

```
Db 449 RLQARYYSIASSKVPNSVHICAVVVEYETKAGRIN-KGVATNWLRAKEPAGENGGRAL 507
QY 877 ITCFISTPQSEFTLPKDPETPLIMVGPGTVAPRFGVQARKQKQKQSLGEAHLFGC 936
Db 508 VPMFVR--KSQFLPFPKATTPVIMVGPGTVAPRFGVQARKQKQKQSLGEAHLFGC 565
QY 937 RSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPRTYYQHVHMEQDGKLIELDDOGAH 995
Db 566 RRSDELYLYREELAQFHRDQALQNLNFAVSREQSH-KVYVQHLLQDREHLWLKLEGGAH 624
QY 996 FYICGDSQMAPAVEATLMKSYADVHOVSADARLWLQLEEKGRYAKDWA 1047
Db 625 IYVCGDARNMARDVQNTFYDVAELGAMEHAQAQVYIKKILMTKGRYSLDWS 676

RESULT 8
US-60-440-068-572
; Sequence 572, Application US/60440068
; GENERAL INFORMATION:
; APPLICANT: NADLER, STEVEN G.
; APPLICANT: CARMAN, JULIE
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE
; FILE REFERENCE: 3053-4191
; CURRENT APPLICATION NUMBER: US/60/440,068
; CURRENT FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 746
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 572
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-440-068-572

Query Match 14.1%; Score 767; DB 7; Length 677;
Best Local Similarity 32.4%; Pred. No. 1.3e-57;
Matches 211; Conservative 113; Mismatches 264; Indels 64; Gaps 23;

QY 444 FVYKAKSKIP----LGGIPSPSTEQS-AKKVRKAENAHNTPLLVLYGSMGTAEGR 498
Db 42 FLFRKKKEEVPETFKIOTLTSSVRESSEFVEKMKKTGRN-----IIVYGSQTGAEEFAN 96
QY 499 DLADIAKSGFAQVATLDSH----AGNLPREGAVLIV--TASY-NGHPPDNKQFVDWL 551
Db 97 RLSKDAHRYGMRGMSADPEEYDLADLSSLPEDNALVYFCMATYEGEDPTDNAQDFYDWL 156
QY 552 DQASADRVKGVYRVSFCGCKGNWATTYQKVP---FIDETLAAGAENIADRGADASDD 608
Db 157 QETDVD--LSGVKFAVGLGNK-----TYEHFNAMGKYVDKRLQELGAORIFELGLGDDGN 211
QY 609 FEETYEWRHMSDVAAYFNLDIENSEDNKSTLSQF---VDSA-----ADMPLAKMH-- 659
Db 212 LEEDFITWRQFPAVCEHFGVEATGESSIRQYELVVHTDIDAAYVMGEMGLKSYEN 271
QY 660 -----GAFSTNVVASKELQOPGSASTRHLEIEL-PKEASYQEGDHLGVIPRNYEGI 710
Db 272 QKPPFDKPNFLAAVTNNRKLQ--GTERHLMHLELDISDSKIRYESGDHVAVYPANDSAL 330
QY 711 VNRVTARFG--LDASQOIRLEAEEKLAHLPLAKTVSVEELLQYVELQDPVTRTOLRAMA 768
Db 331 VNOLGKTLGADLVVMSNLNDESNKKHPFPCPTSYRTALTYYLDTNP-PRTNVLYEL 389
QY 769 AKTVCPHPKVELEALLE-----KQAYKEQVLAKRLTLMLELLEKYPACEMKSEFIALLP 822
Db 390 AQVASEPSEGLRKKMASSGEGKELYLSWVVEARRHILAILQDCPLRPPIHLCCELLP 449
QY 823 SIRPRYISISSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYL-AELQEGDT----- 876
Db 450 RLQARYYSIASSKVPNSVHICAVVVEYETKAGRIN-KGVATNWLRAKEPAGENGGRAL 508
QY 877 ITCFISTPQSEFTLPKDPETPLIMVGPGTVAPRFGVQARKQKQKQSLGEAHLFGC 936
```

Db 509 VPMFVR--KSFRLPKATTPVIMVPGTGVAPFIFGIERAWLRQOGKEVGETLLYYGC 566  
QY 937 RSPHEDYLQOELENAQSEGIIT-LHTAFSRMPNQKTYVOHVMEODGKKLELLDQGAH 995  
Db 567 RRSDEDLRYEELAQPHRDGALTQLNVAFSRQSH-KYVVOHLLKODREHLWKLEBGGAH 625  
QY 996 FYTCGDSQMAPAVEATLMKSYADHVQVSEADARLWLOOLEKRGYAKDVWA 1047  
Db 626 IYVCGDARNKARDVQNTFYDIIVAEIGAMEHAQAVDIKKLMTKGRYSLDWS 677

## RESULT 9

US-10-424-599-187294  
; Sequence 187294, Application US/10424599  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 187294  
; LENGTH: 689  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(689)  
; OTHER INFORMATION: unsure at all xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_140138C.1.pep  
US-10-424-599-187294

Query Match 13.3%; Score 728.5; DB 6; Length 689;  
Best Local Similarity 31.2%; Pred. No. 3.2e-54;  
Matches 195; Conservative 102; Mismatches 256; Indels 73; Gaps 20;  
QY 480 TPLLVLVGNMGTAETARDLAD--IAMSKGAPQVATLDLSHA-----GNLPREGAVL 530  
Db 78 TRVAFIFGQTGTAEFGAKALAEIKARYEKAQVVDLDYAAQEDDEEYEEKLKESLAF 137  
QY 531 IVTASY-NGHPDPAKQFVDWLDQASADEVKGV-----RYSVFGCGDKNWTYQKVPAP 584  
Db 138 FMLATVGDGEPTDAAAFYKWTTEGK-DE-RGIWLXQLYGVFGLGNROY-EHFNKIGKI 194  
QY 585 IDETLAAGAENIADRGADADSDPFEGTYEWEHWMVSDVAAFYFNLDIENSEDNKSTLSL 644  
Db 195 VDEELSEQAKRLVPLGLGDDQSIEDDFVANKESLWSELD-----QLLRDEDDVNTVST 249  
QY 645 QF-----VDSADMPL-----AKMHGAFSTNVVASKELQPGSARST 681  
Db 250 PYKAAIPEYRVVHDSVTSTSCNDNLHNVANGNAVFDIHPCRVNIAAARLHKPESDRSC 309  
QY 682 RLHLELPKEA-SYQEGDHLGVIPRNYEGIVNRVTARFGLDASQOIRLEAEKEKLAHLPL 740  
Db 310 IHLEFPDSTGIYETGDHGVFAENGDEVEAGKLLQODLDLVSFIHTNED--GTPL 367  
QY 741 AKTVSVSVE-----ELQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE---KQA 788  
Db 368 GSSLPPFPFGPCTLRALAHAYADLLNPPRKASIVALAHTSEPSADRLTFLSSPOGKDE 427  
QY 789 YKEQVLAKRLTLMLELEKYPACEMKSEFI-ALLPSIRPRYYSISSSPRVDEKQASITVS 847  
Db 428 YSKWLVSQSLLEVMAEPFSAKPPILGVFAAVAPHQLPRYYSISSSPFSPQKVHTCA 487  
QY 848 VVSGEAWSGYGEYKGIASNY-----LAEIQEDDTITCFISTPQSEFTLPKDPETPLIMV 901  
Db 488 LVCGPPTPG-RIHQVGVCSVMNNAIPLEKSRDCSWAPIFRT---SNFKLPADHSPIIMV 544

QY 902 GPGTGVAPRGRFVQARKQKLEQOQSLGEARHLYFGCRSPHEDYLYOELENAQSEGIIT-L 960  
Db 545 GFGTGLAPRGRFLOERLALKEDAVQLGPALLFGCENRQMDFIYEDDELANEQOGLSEL 604  
QY 961 HTAFSRMPNQKTYVOHVMEODGKKLELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
Db 605 IVTFSR-EGPEKEYVQHKMKMDKAANLWNLISQGGYLVCGDAKGMARDVHRTLHTIVQOQ 663  
QY 1021 HOVSEADARLWLOOLEKRGYAKDVW 1046  
Db 664 ENVDSKAEAIKKLQMDGRYLRDVM 689

## RESULT 10

US-10-425-114-70174  
; Sequence 70174, Application US/10425114  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 70174  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZMFLB73168A03\_FLI.pep  
US-10-425-114-70174

Query Match 13.1%; Score 712.5; DB 6; Length 719;  
Best Local Similarity 30.1%; Pred. No. 8.8e-53;  
Matches 188; Conservative 109; Mismatches 250; Indels 78; Gaps 21;  
QY 484 VLYGNSMGTAETARDLADLADIAISK--GFAPQVATLDLSHA-----GNLPREGAVLIVTA 534  
Db 111 IFFGTGTGTAEFGAKALAEIKARYEKAQVVDLDYAAQEDDEEYEEKLKETVVLFFLA 170  
QY 535 SY-NGHPDPAKQFVDWLDQASADEV--KGVYVFGCGDKNWTYQKVPAPAFIDETLAA 591  
Db 171 TYGDGEPTDAAAFYKWTTEGKEKEVWLKDLKYGIFGLGNROY-EHFNKAVKVDLVEE 229  
QY 592 KGAENIADRGADADSDPFEGTYEWEHWMVSDVAAFYFNLD--IENSED-----637  
Db 230 QGGKRLVPVGLGDDQCIEDDFTAMKELWPE-----LDQLLRDEDDFTGASTPYTAAL 283  
QY 638 -----NKSTLSLQFVDSADMPKAKMHGAFS-----TNVASKELQPGSARSTRH 683  
Db 284 PEYRVVFIKSDLSFQ-----DRSWTLANGTGVIDIQHPCRVNIAARLHKPESDRSCI 339  
QY 684 RLHLELPKEA-SYQEGDHLGVIPRNYEGIVNRVTARFGLDASQOIRLEAEKE-----733  
Db 340 LEFDISGTGLVYETGDHGVFAENSVQVTEVEVERLLDLSPTFFSIHADAEQSPKGGG 399  
QY 734 KLAHLPLAKTVSVE-ELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE---KQAY 789  
Db 400 SLAP-PFSPCTRLRTALLRYADLLNPPKKAALLALASHASDPAEAEERLFLASPSKDEY 458  
QY 790 KEOVLAKRLTLMLELEKYPACEMKSEFI-ALLPSIRPRYYSISSSPRVDEKQASITVS 848  
Db 459 SQMITASQSLLEVMAEPFSAKPPILGVFAAIPRLQPRYYSISSSPKMAPRIHVTCAL 518  
QY 849 VVSGEAWSGYGEYKGIASNYLAEI-----OEQDITTCFISTPQSEFTLPKDPETPLIMV 902  
Db 519 VYGPPTPG-RIHQVGVCSVMNNAIPLEYSSECSWAPIFVR--QSNFKLPADHSPIIMIG 575



Db 477 GCRNRKVDYFENELNNFVENCALSELDMAFSR-EGASKEYVQHKMSQKASDIWNMLSEG 535  
QY 994 AHFYICGDSQMAPAVEATLMKSYADVHOVSADARLWLOOLEEGRYAKDVW 1046  
Db 536 AYLVCGDAGKMAKDVHRTLHTIVQEQNLDSKRAELVYKNLQNSGRYLDDW 588

## RESULT 13

US-10-188-523C-14

; Sequence 14, Application US/10188523C

; GENERAL INFORMATION:

; APPLICANT: Tang, Xiao-Song

; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID

; FILE REFERENCE: BC1009-CIP

; CURRENT APPLICATION NUMBER: US/10/188,523C

; CURRENT FILING DATE: 2002-10-24

; PRIOR APPLICATION NUMBER: US 09/627,216

; PRIOR FILING DATE: 2000-07-27

; PRIOR APPLICATION NUMBER: US 60/147,719

; PRIOR FILING DATE: 1999-08-06

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: MICROSOFT OFFICE 97

; SEQ ID NO 14

; LENGTH: 588

; TYPE: PRT

; ORGANISM: Helianthus tuberosus

US-10-188-523C-14

Query Match 12.9%; Score 705.5; DB 6; Length 588;  
Best Local Similarity 31.9%; Pred. No. 2.5e-52;  
Matches 189; Conservative 92; Mismatches 245; Indels 67; Gaps 19;

QY 499 DLADIAMSGFAPOAVATLDSHAGNLPREGAVLIVTASY-NGHPDPAKQFVDWLDQASAD 557  
Db 18 DLDVY-----ADDEEVAEKFKETFAFFLATVGDGEPTDAAAFYKWFTEG--- 65  
QY 558 EVKGV-----RYSVFGCGDKNWTYQKVPAFIDETLAAGAENIADRGADSDDFEGT 612  
Db 66 DDGKGVLEKHLHYGVFGLGNKQY-EHFNKIALVVDGLTEQAGKRPVPGVGLGDDQSIEDD 124  
QY 613 YEEWEHMSDVAAYFNLDIENSNDKS-----TSLSL-----QFVDSADNPL 655  
Db 125 FSAMEKLWPELDQLL-ID-----EDDKTAATPYTAAIPEYRVFHDKPDPTFSENHSQNG 179  
QY 656 AMHGA-----FSTNVVASKELQPGSARSTRHLEIPLKEA-SYQEGDHLGVIPRYEGIV 711  
Db 180 HTVHDAQHPCRSNVAVKELHTPESDRSCTHLEFDISHGLSYETGDHGVYCEMLIEV 239  
QY 712 NRVTFARFGLDASQQIRLEAEKLAHL-----PLAKTVSVEELLQVVELQDPVTRTOL 764  
Db 240 EEAERKLGLPADTVFSLHIDNEDGTPGLGGPTLQPPFPPTLTKALNTYADLLSSPKKSTL 299  
QY 765 RAMAAKTVCPPHKVLEALLE---KQAYKEQVLAKRLTMELEKYPACEMKFSEFI-AL 820  
Db 300 LALAHASDATEADRLQFLASREGKDETAEMIVANQRSLLLEVMAEFPSAKPLPVFFAAI 359  
QY 821 LPSIRPRYISSSPRVDEKQASITVSVSGEANSYGEYKGIASNY-----LAELOEG 874  
Db 360 APRLOPRYISSSPKMPVNRHIVTICALVY-EKTPGGRIHKGICSTWKNVAPLTENQDC 418  
QY 875 DTITCFISTPOSEFTLPKDPETPLIMVGGTGVAFPGFVQARKOLKQDQSGSLGAHLYF 934  
Db 419 SSAPIFVRT--SNRFLPADPKVPVIMIGPGTGLAPFRGLBRALKESGTELQGSILFF 476  
QY 935 GCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRPNQKTYVQHVWEDQKKLELLDQ 993  
Db 477 GCRNRKVDYFENELNNFVENCALSELDMAFSR-EGASKEYVQHKMSQKASDIWNMLSEG 535  
QY 994 AHFYICGDSQMAPAVEATLMKSYADVHOVSADARLWLOOLEEGRYAKDVW 1046  
Db 536 AYLVCGDAGKMAKDVHRTLHTIVQEQNLDSKRAELVYKNLQNSGRYLDDW 588

## RESULT 14

US-10-424-599-177338

; Sequence 177338, Application US/10424599

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 177338

; LENGTH: 708

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(708)

; OTHER INFORMATION: unsure at all xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_131152C.1.pap

US-10-424-599-177338

Query Match 12.6%; Score 688; DB 6; Length 708;

Best Local Similarity 28.7%; Pred. No. 1.2e-50;

Matches 190; Conservative 114; Mismatches 269; Indels 90; Gaps 21;

QY 447 KAKSKKIP---LGGIPSPSTQSAKVRKKAENAHNTPLLVLYGSMGTAGTARDLADI 503  
Db 73 KAKPLEPPKRVVLEKLEIEVDGKVV-----TILFGTQGTGAEGFAKATAEE 120  
QY 504 AMSK--GFAPOAVATLDSHAGN-----LPREGAVLIVTASY-NGHPDPAKQFVDWLDQ 553  
Db 121 AKARYEKATFRVDDMDYAADDDEVEERFKKETHVLFLLATYGDGEPTDAAAFYKWFTE 180  
QY 554 ASADE---VKGVRYSVFCGDKNWTYQKVPAFIDETLAAGAENIADRGADSDDFE 610  
Db 181 GGEKGEGLWQLHGVFGLGNKQY-EHFNKVAKVVDMLVEQGGKRLVPVGLGDDQDCIE 239  
QY 611 GTYEEWEHMSDVAAYFNLDIENSNDKSITLSLQFVDSA-----ADMPLAKM 658  
Db 240 DDFATWKEELWP-----ALDELLRDEDDATVSTPYTAAVLEYRVVIHDPLEASVDEKKW 293  
QY 659 HGA-----FSTNVVASKELQPGSARSTRHLEIPL-KEASTQEGDHLGVIPRN 706  
Db 294 HNVNGHAIYDAQHPVRANVAVRKELHTPASDRSCTHLEFDISGTGVTYETGDHGVYGEN 353  
QY 707 YEGIVNRVTFARFGLDASQQIRLEAE---KLAHLP-----LAKTVSVEELLQVVEL 755  
Db 354 LSEVVEEAIIRLIGLSPDTYFSIHDDDEGKPRSSGSLPPTFPCTLRTA---LARYADV 409  
QY 756 QDPVTRTOLRAMAAKTVCPPHKVLEALLE---KQAYKEQVLAKRLTMELEKYPACE 811  
Db 410 LSSPKKSALLAALAHASDPSEADRLHLXASAPAGRDEYSEWVIASQRSLLLEVMAEFPSAK 469  
QY 812 MKFSEFI-ALLPSTRPRYISSSPRVDEKQASITVSVSGEANSYGEYKGIASNY--- 867  
Db 470 PPIGVFFAAVAPRLQPRFYSISSSPRMVPRNIRHVTICALVHEKMTGT-RIHGVCSTWKN 528  
QY 868 ---LAELOEGDTITCFISTPOSEFTLPKDPETPLIMVGGTGVAFPGFVQARKOLKEOG 924  
Db 529 SVPLEKSDCQSWAPIFVRT--SNRFLPSDNKVPIMIGPGTGLAPFRGLBRALKKEGG 586  
QY 925 QSLGEAHLFYGCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRPNQKTYVQHVWEDQ 983  
Db 587 AELGPSVLFFCRRNQMDYIYDELSHVNVTGALDELILAFSR-EGPTKEYVQHKMMEKA 645  
QY 984 KKLLELLDQGAHFYICGDSQMAPAVEATLMKSYADVHOVSADARLWLOOLEEGRYAK 1043

Db 646 SEIWSISQAGIYVCGDAKGWARDVHRALHTIIQEQGLDSSKAESMVKNLQTTGRYLR 705

QY 1044 DW 1046  
|||

Db 705 DW 708

RESULT 15

RESULTS  
US-09-661-258-2

US-09-061-238-Z  
; Sequence 2, Application US/09661258

; sequence z, applicat  
; GENERAL INFORMATION:  
GENERAL INFORMATION:

APPLICANT: Stuehr, Dennis J.

APPLICANT: Adak, Subrata

SYNTHASE VARIANTS

FILE REFERENCE: 26473/04028

FILE REFERENCE: 20473/04026  
CURRENT APPLICATION NUMBER: US/09/661,258

; CURRENT REFLECTION NUMBER: 03/0  
; CURRENT FILING DATE: 2000-09-13

; CURRENT FILING DATE: 20  
 ;  
 ; NUMBER OF SEQ ID NOS: 9

; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1; COE1WAKE. F8C  
; SEQ ID NO 2

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; SEQ ID NO 2
; LENGTH: 1429

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; LENGTH: 14
; TYPE: PRT

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; LIFE: FRI  
; ORGANISM: Rattus rattus

US-09-661-258-2

Query Match	12.48;	Score 678;	DB 5;	Length 1429;
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query match  
12.4%, score 0/6, DB 3; length 1429;  
Best Local Similarity  
28.2%; Pred. No. 3.4e-49;

BEST LOCAL SIMILARITY 28.2%; PRED. NO. 3.4E-49;  
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;

QY 457 GIPSPSTEQSAKKVRKAE-----NAHNTPLLVLYGSNMGTAEGTARDLADIA 504

QJ 437 G1F3F51EQSAAKVRKNAE-----NAHN1PFLVLIGSNMGTAEGTARDLADIA 304

ZS / TO CUNOIT FAKKGTOT KATLAEVAFNE SARTTQZATNNAVAHAI LILIAIEIGRSQAHAIDCEIF ///

QV	505	MSGFAPOVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKOF-----	547
----	-----	--	-----

Db 778 KHAFDAKAMSMEEYD|VHLEHEALV|VVTSTFGNGDPP|PENGKEKFGCALMEMRHPNSVOEE 837

DD 778 NHAF DAAHNSMEEIDIVHLEHEALVLVVISIFGNGDPPENGKEFGCALMEMRHPNSVQEE 837

QJ 340 VDWDQ-ASAEVAGVRISVFCCGDKNWTIQKVF 382

Db 838 RKSYKVRFNSVSSYSDSRKSSGDPDLRDNFESTGPIANVRFSVFGLGSR---AYPHFC 893

QY 583 AF---IDETLAAKGAENIADRGADASDDFECTYEEWREHMWSDVAAAYFNL--DIENSED 637

QY J63 AF -- IDEILAAKGAENIADRGADASDDFEGTIEENKREHMWSDVAAAYFNL--DIENSED 637

DD 034 AFGHAYDIUEEELGGERTLNMREGDELCGQEEAFKIWANKVFNAACDVFCVGDDVNTERF 953

638 NKSTLS-----LOFVDSAADMP--LAKMH--GAFSTNVVASKELOOPGSARSTR 682 QV

db 954 NNSLISNDRSWKRNKFRITYVAEAPDI.TOGI.SNVHKKRVSAARI.TSPONT.OSPKFSRSTI 101

DD 934 NNSLISNDRKSWAKRNKFRLLTYVAEAPDLTQGLSNVHKRRVSAARLLSRQNLQSPKFSRSTI 101

QY 003 HUEIEL--PREASIQEGDHLGVIPRNYEGIVNRVTARF--GLDASQIRLEAEEERLAHL 738

db 1014 FVRLHTNGNOETQYOPGDHTGVPEGNHEDIYNALIERLEDAPPANHVVKVEMTEERTAL. 107

OV 739 PLAKTVSVEELL-----QVVELODPVTRTOIRAMAAKTVCPPHKVLEI.EI.E-KO 787

QY 739 PLAKIVSVEELL-----QYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE-KQ 787

DB 10/4 GVISNWRDESRLLPFCIFQAFKRYLYLDITTPPTPLQLQQFEASLATNEKEKQRLTVLSKGLQ 113

OV 788 AYKEOVI AKRITMTIETIEKY PACEMKFEFEETAILPSIBDPVYSSSSPPVDEKQASTYVS 847

1134 EYEFNKWGKNPTMVEVTFEEFPSTOMPATLITOLSIORPPVYSTSSSPDM:PDREYHI TYVA 110

DB 1134 EYEWKWGKNPTMVEVLEEFPSIQMPATLLTLQLSLLQPRYYSISSSPDMPDEVHLTVA 119

QY 1023 VSEADARLWLQQLLEEKGRYAKDV 1046

0401 MAGNETYVEETQDTMTVYUACA CZAT  
::| | : | ::||  
::| | : | ::||

Search completed: May 29, 2003, 08:26:31  
Job time : 58 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 29, 2003, 08:26:36 ; Search time 49 seconds  
(without alignments)  
2056.099 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 5457

Sequence: 1 TIKEMPQKTFGELKNLPL.....RLWLOLEKGRYAKDVWAG 1048

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5457	100.0	1049	1 A34286	NADPH-ferrihemopro
2	3314	60.7	1061	2 D69799	cytochrome P450 /
3	3281.5	60.1	1054	1 A69975	NADPH-ferrihemopro
4	777.5	14.2	678	1 RDR704	NADPH-ferrihemopro
5	769	14.1	677	1 RDR704	NADPH-ferrihemopro
6	769	14.1	679	2 A25505	NADPH-ferrihemopro
7	767	14.1	677	2 A60557	NADPH-ferrihemopro
8	761.5	14.0	678	2 S27158	NADPH-ferrihemopro
9	739.5	13.6	692	2 T05582	NADPH-ferrihemopro
10	737.5	13.5	681	2 T14903	NADPH-ferrihemopro
11	735.3	13.5	671	2 A56592	NADPH-ferrihemopro
12	723	13.2	601	2 A28577	NADPH-ferrihemopro
13	723	13.2	690	2 A47298	NADPH-ferrihemopro
14	711.5	13.0	683	2 T10720	NADPH-ferrihemopro
15	711	13.0	692	2 S37159	NADPH-ferrihemopro
16	709	13.0	711	2 T14081	NADPH-ferrihemopro
17	706	12.9	705	2 T10723	NADPH-ferrihemopro
18	705.5	12.9	590	2 S37157	NADPH-ferrihemopro
19	705	12.9	699	2 T14904	NADPH-ferrihemopro
20	702.5	12.9	712	2 S21531	NADPH-ferrihemopro
21	702	12.9	714	1 S31502	NADPH-ferrihemopro
22	684.5	12.5	662	2 G88451	protein K102.6 [1
23	683.5	12.5	1147	1 I56375	nitric-oxide synth
24	679	12.4	1429	2 JN0509	nitric-oxide synth
25	678	12.4	1429	1 S16233	nitric-oxide synth
26	677.5	12.4	1147	1 S38253	nitric-oxide synth
27	675.5	12.4	1147	1 I53165	nitric-oxide synth
28	675.5	12.4	1147	2 JC5029	nitric-oxide synth
29	675	12.4	1433	2 G01946	nitric-oxide synth

ALIGNMENTS

RESULT 1

A34286

NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Bacillus megaterium  
N;Contains: NADPH-ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (C;Species: Bacillus megaterium  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
C;Accession: A34286; S43653

R;Ruettinger, R.T.; Wen, L.P.; Fulco, A.J.

J. Biol. Chem. 264, 10987-10995, 1989

A;Title: Coding nucleotide, 5' regulatory, and deduced amino acid sequences of P-450-

A;Reference number: A34286; MUID:89291834; PMID:2544578

A;Accession: A34286

A;Molecule type: DNA

A;Residues: 1-1049 <RUE>

A;Cross-references: GB:J04832; NID:J142797; PIDN:AA87602.1; PID:G142798

R;Munro, A.W.; Lindsay, J.G.; Coggin, J.R.; Kelly, S.M.; Price, N.C.

FEBS Lett. 343, 70-74, 1994

A;Title: Structural and enzymological analysis of the interaction of isolated domains  
A;Reference number: S43653; MUID:94215710; PMID:8163021

A;Accession: S43653

A;Molecule type: protein

A;Residues: 430-439;441-496 <MUN>

C;Genetics:

A;Gene: CYP102

C;Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin  
C;Keywords: chromoprotein; electron transfer; FAD; flavoprotein; FMN; heme; iron; met  
F;862-423/Domain: cytochrome P450 homology <P45>

F;483-1046/Domain: NADPH-ferrihemoprotein reductase homology <FEH>

F;485-622/Domain: flavodoxin homology <FLX>

F;401/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 5457; DB 1; Length 1049;  
Best Local Similarity 100.0%; Pred. No. 3.1e-298;  
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TIKEMPQKTFGELKNLPLINTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60
DB	2	TIKEMPQKTFGELKNLPLINTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 61
QY	61	ACDESFPDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMGYHAMV 120
DB	62	ACDESFPDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNILLPSFSQAMGYHAMV 121
QY	121	DIAVOLVQWERNLADEHIEVPEDMTLTDITGLCGFNYSFVSDQHPFTTSMVRA 180
DB	122	DIAVOLVQWERNLADEHIEVPEDMTLTDITGLCGFNYSFVSDQHPFTTSMVRA 181
QY	181	LDEAMNKLQANPDDPAYDENKQFOEDIKVMNDLVKIIADRKASGEQSDLLTTHMLNG 240
DB	182	LDEAMNKLQANPDDPAYDENKQFOEDIKVMNDLVKIIADRKASGEQSDLLTTHMLNG 241
QY	241	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAAARVLVD 300

|||||  
242 KDPTGEPDDEIRYQIITFLIAGHETTSGLLSFALYLVNPNHVLQKAAEAAARVLD 301  
QY PVPYSQVQKLVGVNVLNEALRLWPTAPAFSLYAKEDTVLGGEPLEKGDDELVLIPOL 360  
Db PVPYSQVQKLVGVNVLNEALRLWPTAPAFSLYAKEDTVLGGEPLEKGDDELVLIPOL 361  
QY HRDKTIWGDVVEEFPERFENPNSAIPQHAFFKPGNGQACIGQGFALHEATLVLMMLKH 420  
Db HRDKTIWGDVVEEFPERFENPNSAIPQHAFFKPGNGQACIGQGFALHEATLVLMMLKH 421  
QY FPFEDHTNVELDIKETLTKPGFVVKAKSKKIPGLGIPSPSTESAKKVRKAENAHNT 480  
Db FPFEDHTNVELDIKETLTKPGFVVKAKSKKIPGLGIPSPSTESAKKVRKAENAHNT 481  
QY PLVLVYSGNMGTAEGTARDLADIAKSGFAPOVATLDSHAGNLPREGAVLIYVTSNGHP 540  
Db PLVLVYSGNMGTAEGTARDLADIAKSGFAPOVATLDSHAGNLPREGAVLIYVTSNGHP 541  
QY PNAKQFVDWLQASADEVKGVYRVSFGCGDKNNWATTYQKVPFADITELAAKGAENIADR 600  
Db PNAKQFVDWLQASADEVKGVYRVSFGCGDKNNWATTYQKVPFADITELAAKGAENIADR 601  
QY GEADASDDPEGTYEWRHWNWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPKMHG 660  
Db GEADASDDPEGTYEWRHWNWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPKMHG 661  
QY AFSTNVVASKLQOQPGSARSTRHLELTELPEKASYQEGDHLGVIPRNYEGIVNRYTARFGL 720  
Db AFSTNVVASKLQOQPGSARSTRHLELTELPEKASYQEGDHLGVIPRNYEGIVNRYTARFGL 721  
QY DASQQLRLAEAEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAAKTVCPKHKVEL 780  
Db DASQQLRLAEAEKLAHLPLAKTVSVEELLQVVELQDPVTRTQLRAMAAKTVCPKHKVEL 781  
QY EALLEKQAYKEQVLAKRLTLMLELKY PACEMKSEFIALLSIRPRYISISSPRVDEK 840  
Db EALLEKQAYKEQVLAKRLTLMLELKY PACEMKSEFIALLSIRPRYISISSPRVDEK 841  
QY QASITVSVYSGGAWSGYGEYKGIASNYLAELQEGDTITCFSTPOSEFTLPKDPETPLIM 900  
Db QASITVSVYSGGAWSGYGEYKGIASNYLAELQEGDTITCFSTPOSEFTLPKDPETPLIM 901  
QY VPGGTGVAPFRGVQARKQKQOGLSGEALHYFCGRSPHEDYLYQOEELENAQSEGIITL 960  
Db VPGGTGVAPFRGVQARKQKQOGLSGEALHYFCGRSPHEDYLYQOEELENAQSEGIITL 961  
QY HTAFSRMPNQPITYYQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
Db HTAFSRMPNQPITYYQHVMEQDGKLIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1021  
QY HQVSEADARLWQLEEKGRYAKDVWAG 1048  
Db HQVSEADARLWQLEEKGRYAKDVWAG 1049

## RESULT 2

D69799  
cytochrome P450 / NADPH-cytochrome P450 r homolog yeto - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 28-Jul-2000  
C:Accession: D69799  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
C.; Bron, S.; Brouillet, C.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serod

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toqnoni, A.; Tosato, V.; Uchiya  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Damchin, A.  
A:Title: The complete genome sequence of the gram-positive bacterium Bacillus subtili  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: D69799  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1061 <KUN>  
A:Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12544.1; PID:g26330  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yeto  
C:Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin  
C:Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein  
F:264-425/Domain: cytochrome P450 homology <P45>  
F:493-1057/Domain: NADPH-ferredoxin reductase homology <FEH>  
F:495-632/Domain: flavodoxin homology <FLX>  
F:403/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 60.7%; Score 3314; DB 2; Length 1061;  
Best Local Similarity 59.5%; Pred. No. 5.7e-178; Indels 12; Gaps 6;  
Matches 628; Conservative 156; Mismatches 259;

QY 5 MPQPTFGELKMLPLNTDKPVQALMKIADELGEIFKFEAPGRVTRYSLSRLKEACDE 64  
Db 7 IPQPTFGPLGNLPLIDKDKPTLSLKLAEQGFQIHTPAGTITVSSGHELKVECD 66  
QY 65 SRFDKNLQALKFVRDFAAGLFTSWTHKKNKKAHNLPLPSQOAMGYHAMVVDIAV 124  
Db 67 ERFDSIEGALEKVRFAFGDGLFTSWTHKKNKKAHNLPLPSQOAMGYHAMVVDIAV 126  
QY 125 QLVQKWERLNADHELEVPEDMTLRLDTLGLCGVYRNSFYRSDPHPTSMVRLDEA 184  
Db 127 QLIQKWARLNADHELEVPEDMTLRLDTLGLCGVYRNSFYRSDPHPTSMVRLDEA 186  
QY 185 MNKLQANPDDPAYDENKQFQEDIKVNDLVKIIADKASGEQSD-DLLFHLNGKDP 243  
Db 187 MHQMLQVQDKLWRTKQFQYDIQTFSLVDSIIAERRANGDQDEKLLARMLNVEDP 246  
QY 244 ETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYLVNPNHVLQKAAEAAARVLDV 303  
Db 247 ETGEKLDDEIRYQIITFLIAGHETTSGLLSFALYLVNPNHVLQKAAEAAARVLDV 306  
QY 304 SYKQVQKLVGVNVLNEALRLWPTAPAFSLYAKEDTVLGGEPLEKGDDELVLIPOL 363  
Db 307 TYKQVLELYIRMLNLSRLWPTAPAFSLYAKEDTVLGGEPITNDIRISVLIPQLHRD 366  
QY 364 KTIWGDVVEEFPERFENPNSAIPQHAFFKPGNGQACIGQGFALHEATLVLMMLKH 423  
Db 367 RDWKGDAEERFPERFEHQDQVPHAYKPFNGQACIGMQLHEATLVLMMLKLYFTL 426  
QY 424 EDHTNVELDIKETLTKPGFVVKAKSKKIPGLGIPSPSTESQSA---KVRKAENA--- 477  
Db 427 IDHENYELDIKETLTKPGFVVKAKSKKIPGLGIPSPSTESQSA---KVRKAENA--- 486  
QY 478 --HNTPLVLYSGNMGTAEGTARDLADIAKSGFAPOVATLDSHAGNLPREGAVLI 535  
Db 487 GLNNRPLVLYSGDGTAGVARELADTASLHGVTKTAPLNDRLGKLPKEGAVIVTSS 546  
QY 536 YNGHPDPAKQFVDWLQASADEVKGVYRVSFGCGDKNNWATTYQKVPFADITELAAKGA 595  
Db 547 YNGKPPSNAGQFVQWLQKPELGVHVFVFGCGDHNNWASTYQVVPVRFIDQLAEKAT 606  
QY 596 NIADGEADASDDPEGTYEWRHWNWSDVAAYFNLDI-ENSEDNKSTLSLQFVDSAADMP 654  
Db 607 RFSARGEVSDGDFEGDGLDEKMSWADAIRAFGLLENADKERSSTLSLQFVRLGSP 666  
QY 655 LAKMHGAPSTNVVASKLQOQPGSARSTRHLELTELPEKASYQEGDHLGVIPRNYEGIVN 714  
Db 667 LARSVEASHASTAENRELQSDSRSTRHLELTELPELPPVVEYQEGDHLGVLPKNSQTVSRI 726  
QY 715 TARFGLDASQQLRLAEAEKLAHLPLAKTVSVEELLQV-VELQDPVTRTQLRAMAAKTV 773



727	LHRFGUKGTDQVTL	SASGRAGHLP	GRPVSUHL	LUSV	VEQEA	TRAQIR	ELASFTVC	786
774	PPHKVEALLEKQAY	KEQVLA	KRLM	LELEKYP	ACEMK	FSFTI	ALLPSIRPY	833
787	PPHRELELSAGVY	QEQLK	KRISML	DLLEY	ACDMP	FEFLE	LLPLKPRY	846
834	SPRVDSQASITV	SVVSG	EWMSY	GEYK	GIASNY	LAELQ	EGDPTIT	893
847	SPRVNPROASIT	VGVYRG	PAWSGR	GEYRG	VASND	LAERQ	AGDDVVM	906
894	PETPLTMVGP	TGVP	PRFGV	QARKOL	KEGOSI	GEAHLY	FGCRSP	953
907	PETPIITMVGP	TGVP	PRFGV	LQARDV	LKREGT	LGEAHLY	FGCRN	965
954	SEGIITLHTAF	SMPNQPT	TYGVH	MEQDC	GKLI	ELLDDQ	GAHFYIC	1013
966	KDGI	VIVHTAF	SKEG	MPTYV	QHLMA	DQADT	LISIL	1025
1014	MKSYAD	VHGVSE	ADARL	WTQOL	EEKRYA	KDVWAG	1048	
1026	KRAYAV	HGTGEQ	EQAQ	NWLRH	LQD	TYGM	KDVWAG	1060

### RESULT 3

A69975  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - *Bacillus subtilis*  
N:Contains: NADPH-ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (EC 1.10.3.3)  
C:Species: *Bacillus subtilis*  
C|Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 03-Jun-2002  
C|Accession: A69975  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertone,  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chentouf,  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen-  
bach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,  
Y. M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,  
Rieger, M.; Rivolta, C.; Rocha, R.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serono,  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstap, P.; Tononni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A>Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: A69975

Query Match	60.1%	Score 3281.5;	DB 1;	Length 1054;
Best Local Similarity	58.5%;	Pred. No. 3.8e-176;		
Matches 614;	Conservative 173;	Mismatches 254;	Indels 9;	Gaps 6;
Qy	5	MPQKTEGELKNPLPLNTDPVQALMKIADDELGEIFKEFAPGRVTRYLSQRILKEACDE	64	
		:      :     :	:	:
Db	7	IPOKYTGPLKNPLHLEKEQLSQSLMRIADLGPFIREFDPPGVSSVFVSHNLVAEVCDE	66	
		:      :     :	:	:
Qy	65	SREDKNLSQALKFVRDFPAGDLGTSWTHENXNWKAKHNILLPSFSQAAMGYHAMVDIAV	124	
		:      :     :	:	:
Db	67	KREDKNLGKGLQVREGDGGLTSTWTFHWQKAHRILLPSFSQAKMGYHSNMMLDIAT	126	
		:      :     :	:	:

[illegible]

## RESULT 4

RDR0704  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - rat  
N:Alternate names: NADp-cytochrome P450 reductase  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 27-Nov-1985 #sequence\_revision 27-Nov-1985 #text\_change 03-Jun-2002  
C:Accession: A36073; A00402; A25813  
R:Porter, T.D.; Beck, T.W.; Kasper, C.B.

Biochemistry 29, 9814-9818, 1990  
 A;Title: NADPH-cytochrome P-450 oxidoreductase gene organization correlates with structure  
 A;Reference number: A36073; MUID:91104889; PMID:2125483  
 A;Accession: A36073  
 A;Molecule type: DNA  
 A;Residues: 1-678 <P02>  
 A;Cross-references: GB:J05291  
 R;Porter, T.D.; Kasper, C.B.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 973-977, 1985  
 A;Title: Coding nucleotide sequence of rat NADPH-cytochrome P-450 oxidoreductase cDNA and  
 A;Reference number: A00402; MUID:85140278; PMID:3919392  
 A;Accession: A00402  
 A;Molecule type: mRNA  
 A;Residues: 1-678 <P0R>  
 A;Cross-references: GB:M10068; NID:g203872; PIDN:AAA41064.1; PID:g203873  
 R;Murakami, H.; Yabusaki, Y.; Ohkawa, H.  
 DNA 5, 1-10, 1986  
 A;Title: Expression of rat NADPH-cytochrome P-450 reductase cDNA in Saccharomyces cerevisiae  
 A;Reference number: A25813; MUID:86163762; PMID:3082610  
 A;Accession: A25813  
 A;Molecule type: mRNA  
 A;Residues: 1-678 <MUR>  
 A;Cross-references: GB:M12516; NID:g203878; PIDN:AAA41067.1; PID:g203879  
 C;Comment: This enzyme, a membrane-bound flavoprotein containing one molecule each of FMN  
 and to bacterial flavodoxins.  
 C;Genetics:  
 A;Introns: 60/2; 76/3; 119/3; 169/3; 211/2; 241/2; 313/2; 353/1; 413/3; 463/3; 55  
 C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein  
 C;Keywords: electron transfer; endoplasmic reticulum; FAD; flavoprotein; FMN; membrane protein  
 F;1-56/Domain: membrane-bound #status predicted <MEM>  
 F;71-227/Domain: FMN binding #status predicted <FMN>  
 F;80-676/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
 F;82-224/Domain: flavodoxin homology <FLX>  
 F;84-95/Region: FMN-phosphate binding #status predicted  
 F;267-326,452-477/Domain: FAD binding #status predicted <FAD>  
 F;293-296/Region: FAD-pyrophosphate binding #status predicted  
 Query Match 14.2%; Score 777.5; DB 1; Length 678;  
 Best Local Similarity 32.2%; Pred. No. 6.4e-36;  
 Matches 211; Conservative 111; Mismatches 263; Indels 71; Gaps 23;  
 QY 444 FVYKAKSKTIP-----LGGIPSPSTEQS-AKKVKKKAENAHNTPLLVLYGSGNMGTAAGTAR 498  
 DB 42 FIFRKKKEELPEPSKLTAPPVKVESFVEKMKKTGRN-----IIVFGSQTGTAEFAN 96  
 QY 499 DLADIAMSGEAPQVATLDLSDH-----AGNLP--EGAVLITASY-NGHPPDNAKQFVDWL 551  
 DB 97 RLSKDAHYGRMGMSADPEYDLADLSSLPEDIKSLVFCMATYGGDPTDQAQDFYDNL 156  
 QY 552 DQASADEVGVRYSVFGCGDKNWTYQKVA---FIDETLAAGAENIADGEADASD 608  
 DB 157 QETDQVD-LTGKFAVFLGNK-----TYEHFNAMGKYVDQRLQGLGAORIFELGLGDDGN 211  
 QY 609 FECTYEERHMHMSDVAAYFNLDIENSNDKSTLSLQFVDSADMPKAKWH----- 659  
 DB 212 LEEDFTWRQFPAPVCEFFGVATGEESIRQYELVWHE---DMDVAVTYGEMGRKLS 268  
 QY 660 -----GAFSTNVYASKELOQPGSARSTRHLEIEL-PKEASVQEGDHLGVIPRNY 707  
 DB 269 YENQKPPFDKAPNPLAAVTAANRLNQ-GTERHLMHLELSDSKIRYSGDHVAVYPAND 327  
 QY 708 EGVNVRVTRFG---LDASQIRLEAEEELKLAHLPLAKTVSVEELQYVLOQDPVTRQLR 765  
 DB 328 SALVNIQETGLADLVIMSLNLDSESNKHPFPCTTYRTALTYYLDTNTP-PRTNVL 386  
 QY 766 AMAAKTVCP-----HKVELEALLKQAYKEQVLAKRITMLELLEKYPACEMKSEFTA 819  
 DB 387 YELAQVASESEGEHLHKMASSGEGEKLYLSWVVEARRHIALQDYSLRPPIDHLC 446  
 QY 820 LLPISIRPYISISSPRVDEKQASITVSVSGEANSVGYEYKIASNYL-AELQEGDT-- 876  
 DB 447 LLPLQARYYSIASSSKVHPNSVHICAVAVEYEAKSGRYN-KGVATSWLRAKEPENGSG 505

877 ---ITCFISTPQSEFTLPKDPETPLIMVPGTGVAPRGFQVQARKOLKEQOSILGEAHL 933  
 DB 506 RALVPMFVR--KSQFRLPFKSTTPVIMVGGTGIAPFMGFIQERAWLREGCKEVEGTELLY 563  
 QY 934 FGRSPHEDYLYQDELENAQSEGIIT-LHTAFSRMPNQPKTYVQYHNEQDGKGLIELDQ 992  
 DB 564 YGCRSDEYLYREELARFHKDGLQNLNFAFSK-EQAHKVYVQVHLLKRDREHLWLKLIHE 622  
 QY 993 -GAHFYICGDSOMAPAVEATLMKSVADYHVNQSEADARLWLOLEKRGYAKDYWA 1047  
 DB 623 GGAHYVCGDARNMAKDQVNTFYDVAEFGPMHTQAVDYVKKLMTKGRYSLDVWS 678  
 RESULT 5  
 RDPG04  
 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - pig  
 N;Alternate names: NADP-cytochrome P450 reductase  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 04-Dec-1986 #sequence\_revision 03-Feb-1994 #text\_change 03-Jun-2002  
 C;Accession: A25584; A00403  
 R;Hanlu, M.; Iyanagi, T.; Miller, P.; Lee, T.D.; Shively, J.E.  
 Biochemistry 25, 7906-7911, 1986  
 A;Title: Complete amino acid sequence of NADPH-cytochrome P-450 reductase from porcine  
 A;Reference number: A25584; MUID:87101085; PMID:3099837  
 A;Accession: A25584  
 A;Molecule type: protein  
 A;Residues: 1-677 <HAN>  
 R;Vogel, F.; Lumper, L.  
 Biochem. J. 236, 871-878, 1986  
 A;Title: Complete structure of the hydrophilic domain in the porcine NADPH-cytochrome  
 A;Reference number: A00403; MUID:87075664; PMID:3098240  
 A;Accession: A00403  
 A;Molecule type: protein  
 A;Residues: 56-162, 'S', '164-173', 'D', '175-338', 'A', '340-377', 'D', '379-399', 'E', '401-445', 'L', '44  
 C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihem  
 C;Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; flav  
 F;76-126/Domain: FMN binding <FMN>  
 F;79-675/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
 F;81-223/Domain: flavodoxin homology <FLX>  
 F;451-476/Domain: FAD binding <FAD>  
 F;1/Modified site: acetylated amino end (Gly) #status experimental  
 Query Match 14.1%; Score 769; DB 1; Length 677;  
 Best Local Similarity 31.9%; Pred. No. 1.9e-35;  
 Matches 224; Conservative 109; Mismatches 275; Indels 94; Gaps 27;  
 QY 401 IGOQFALHEAT-----LVLGMMLKHDFEDHTNY--ELDIKETLT-LKPEGFVYKAKS 450  
 DB 15 VAEVSLFSATDMVFLSLIVGLTYWFIPIRKKKDEVPFESKTIETTTSSVKDSFV----- 69  
 QY 451 KKIPLGGIPSPSTEQSAAKVRKKAENAHNTPLLVLYGSGNMGTAEGTARDLADTAMSKGFA 510  
 DB 70 -----EKMKKTGRN-----IIVFGSQTGTAEFANRLSKDAHYGMR 107  
 QY 511 PQVATLD-----SHAGNLP--EGAVLI-VTASY-NGHPPDNAKQFVDWLQASADEYKGVYR 563  
 DB 108 GMAADPEEYDLSDLSLPEIENALAVFCMATYGGDPTDQAQDFYDNLQADVD-LTGK 166  
 QY 564 YSVFEGCGDKNWTYQKVA---FIDETLAAGAENIADGEADASDDDECTYEWEHEM 620  
 DB 167 YAVFVLGNK-----TYEHFNAMGKYVDKRLQGLGAORIFDLGLGDDGDNLEEDFITWRQF 222  
 QY 621 WSDVAAYFNLDIENSNDKSTLSLQF-----VDSAA-----DMLAKMKHGFAS 663  
 DB 223 WFAVCEHFGVATGEESIRQYELVHTDMDTAVVYTGEMGRKLSYENQKPPFDKAPNPL 282  
 QY 664 TNVASKELQPGSARSTRHLEIEL-PKEASVQEGDHLGVIPRNYGVNRTARFGLDA 722  
 DB 283 AVYTTNRLNQ-GTERHLMHLELSDSKIRYSGDHVAVYPANDSALVNLQELIGTDL 341  
 QY 723 SQOI---RLEAEEELKLAHLPLAKTVSVEELQYVLOQDPVTRQLRAMAKTVCPKHYE 779  
 DB 342 DIVMSLNLDSESNKHPFPCTTYRT-ALTYLDTNTPRNVLYELAQYASESESEQ 400

[illegible]

A; Cross-I

References: EMBL:AL033330



## RESULT 11

A56592  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - house fly  
N:Alternate names: NADPH-cytochrome P450 reductase; P450 reductase  
C:Species: Musca domestica (house fly)  
C:Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 03-Jun-2002  
C:Accession: A56592  
R:Koener, J.F.; Carino, F.A.; Feyerelsen, R.  
Insect Biochem. Mol. Biol. 23, 439-447, 1993  
A:Title: The cDNA and deduced protein sequence of house fly NADPH-cytochrome P450 reductase  
A:Reference number: A56592; MUID:93284260; PMID:8508186  
A:Accession: A56592  
A>Status: preliminary  
A:Molecule type: DNA; mRNA  
A:Residues: 1-671 <KOE>  
A:Cross-references: GB:119897; NID:G308945; PID:AAA29295.1; PID:G308946  
A:Note: sequence extracted from NCBI backbone (NCBI:134359, NCBI:134361, NCBI:133605)  
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein  
C:Keywords: flavoprotein; membrane protein; NADP; oxidoreductase  
F:77-669/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F:79-221/Domain: flavodoxin homology <FLX>

Query Match 13.5%; Score 735.5; DB 2; Length 671;  
Best Local Similarity 30.0%; Pred. No. 1.4e-33;  
Matches 199; Conservative 123; Mismatches 255; Indels 87; Gaps 25;

QY 444 FVYAKSKKIPIGG-----IPSPTEQSA--KKVRKKAENAHNTPLLVXGNNMGTA 494  
DB 35 FMRSRKKKEAPISYSIQPTTVSTVSTTENSFIKLLK-----ASGRSLVVFYGSQTGTA 89  
QY 495 GTARDIADAM---SKGFA--QVATLDS--HAGNLPREGAVLIVTASTNGHPPDNKAF 547  
DB 90 EFAGRLAKGLRYRMKGVADPECDMEELLQMDIPNSLAVFLCYATYGEQDPTNAMEF 149  
QY 548 VDWLQASADEKGVYSGVCGDKNWTYQKVPFIDETLAAGAENIADRGASD 607  
DB 150 YEWITNGEVD--ITGLNVAFGLNKTY--EYHNKVALYVDKRLLEAGVTFELGDDDA 207  
QY 608 DFEQTYEWEHMSDVAAYFNLDIENSEDNKSTLSQFVDSAADMP-----LAKMH- 659  
DB 208 NIEDDFTWKDRFVPSVCFDFG--IEGSGEVLVLRQFLLEQPDVQPDRIYTGTEARLHS 265  
QY 660 -----GAFSTNVASVELQPGSARSSTRHLEIEP--KEASVQEGDHLGVIPRY 707  
DB 266 MNQRPPFPAKPPFLASVIVNRELHK--GGGRSCMHIELDIDGSKRYDAGDHIAFYIND 324  
QY 708 EGIYVNRV--TAREGLD--ASQQLRLEAEKLAHLP-----LAKTVSVE 747  
DB 325 KILVEKLGKLCDAALDVTESLNTDSSKKHPFPCTTYRTALHYLEITAIPRTHILK 384  
QY 748 ELQVYELQDPVTRTQLRAMAAKTVCPPHKVEALELLEKQAYKEQVLAKRLTLMLELKY 807  
DB 385 ELAEY--CSDEKDEKFLRNASTIT--PE-----GREKYONQNSRNIVHLEIDI 431  
QY 808 PACEMKFSEFIALLPSIRPRYSISSSPVDEKQASITVSVSGEAWSGYGEYKIASNY 867  
DB 432 KSCRPPIDHICELLRLQPRYSISSSKSLYPTNWHITAVLYOYETPTGRVN--KGVATSY 490  
QY 868 LAELQD--GDT--ITCFISTPQSEFTLPKDPETPLIMVPGTGVPAPRGVQARKOLKEOG 924  
DB 491 MKEKNPSGEVAVPVFIR--KSQFLPTKSEIPLIMVPGTGGLAPFRGIQRFQRLDGG 548  
QY 925 QSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAFSRMPNPKTYVQHVMEQDGK 984  
DB 549 KVVGDITLYFGCRKKDEDFIYREELEQYVQNGTTLTKTAFSR--DQOEKIYVTHLIEQDAD 607  
QY 985 KLIELL--DQGAHFYICGDSQNAPEATLMKSYADVHOVSEADARLWLOOLEEGRYAK 1043  
DB 608 LIWKVIGEQGHFYICGDAKNMAVDVNRILVILSTKGNMNSDAVQYIKKMEAKRYSA 667

1044 DYWA 1047  
DB 668 DWWS 671

## RESULT 13

A47298  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - mung bean  
N:Alternate names: NADPH-cytochrome P450 reductase

## RESULT 12

A28577  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - brown trout (fragments)  
C:Species: Salmo trutta (brown trout)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 03-Jun-2002  
C:Accession: A28577  
R:Urenjak, J.; Linder, D.; Lumper, L.  
J. Chromatogr. 397, 123-136, 1987  
A:Title: Structural comparison between the trout and mammalian hydrophilic domain of  
A:Reference number: A28577; MUID:88008061; PMID:3116019  
A:Accession: A28577  
A:Molecule type: protein  
A:Residues: 1-601 <RUE>  
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein  
C:Keywords: flavoprotein; NADP; oxidoreductase  
F:25-599/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F:27-169/Domain: flavodoxin homology <FLX>

Query Match 13.2%; Score 723; DB 2; Length 601;  
Best Local Similarity 30.2%; Pred. No. 6.1e-33;  
Matches 195; Conservative 106; Mismatches 239; Indels 106; Gaps 21;

QY 459 PSPSTEQSA--KKVRKKAENAHNTPLLVYSGNMGTAEGTARDIADIAKSGFAPQVATL 516  
DB 5 PAPSTQSTFIEKMKTKGRN-----IVFYGSQTGTGEEFANRLSKDAHRYGMSNAADP 59  
QY 517 D-----SHAGNLPREGAVLIV--TASY--NGHPDPNKAQFVDMWLDQASADKVGVRYSVFGC 569  
DB 60 EYDMSLSRLAEIGNSLAIFCMATYEGDPDYNADQFYDWL--QETDGLSGVNYVDFAL 118  
QY 570 GDKNWTYQKVPFIDETLAAGAENIADRGASDDEFGTYEWEHMSDVAAYFN 629  
DB 119 GDKTY--EYHNAGAVYDKLEELGAKRVEDLGMGDDGDLNLEDFYTWROQFWPAMEHFG 177  
QY 630 LDENSEDNKSTLSQFVDSAADMPLAKMH-----GAFSTNVAS 669  
DB 178 VEASGDSVROVELK--EHNDINNMKVYTGELGRKLSFETQKPPDAKNPFLADPTVN 234  
QY 670 KELQPGSARSSTRHLEIEP--KEASVQEGDHLGVIPRYEGIVNRVTAERGLDASQIIRL 728  
DB 235 RKLKAGELHK--MHLEVDITGSKIRYESGDHVAVYPTNNTVIVNRUGQILGVDLDSVISL 293  
QY 729 EAEERK-----LAHPLAKTVSVEELQY--VELQDPVTRTQLR 765  
DB 294 NNLDESNKKHPFPCTTYRTALTHTYLDIHP--RTNVLVELAQYATDLKQDENTDMA 351  
QY 766 AMAATVCPPHKVELEALEKQAYKEQVLAKRLTLMLELLEKYPACEMKFSEFIALLPSIR 825  
DB 352 SSAPE-----GKALYQSFVLEDNRNLAILEDLPSLRPPIDHLCCLMPRIQ 397  
QY 826 PRYSSISSPRVDEKQASITVSVSGEAWSGYGEY--KGIASNYLAELQEGDTITCFIST 883  
DB 398 ARYTSASSKVPHPNSIHICAVLV-----EYTKGAVTTLKYLIR----- 437  
QY 884 PQSEFTLPKDPETPLIMVPGTGVPAPRGVQARKOLKEQSGSLGEAHLYFGCRSPHEDY 943  
DB 438 -KSQFLRPFKAPNPVIMVPGTGVIAPFMGFIQERGLWKSKEGVEGTLYVCCGRKKEEDY 496  
QY 944 LYQEELENAQSEGIITLHTAFSRMPNPKTYVQHVMEQDGKLL--IELDQGAHFYICGD 1001  
DB 497 LYQEELENAQSEGIITLHTAFSRMPNPKTYVQHVMEQDGKLL--IELDQGAHFYICGD 555  
QY 1002 GSQMAPAVEATLMKSYADVHOVSEADARLWLOOLEEGRYAKDVA 1047  
DB 556 ARNARDVQTAPEYAEELGGMTRTQATDIYIKLTKGRYSQDVWS 601

C:Species: *Vigna radiata* (mung bean)  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 03-Jun-2002  
C:Accession: A47298  
R:Shet, M.S.; Sathasivai, K.; Arlotto, M.A.; Mehdi, M.C.; Estabrook, R.W.  
Proc. Natl. Acad. Sci. U.S.A. 90, 2890-2894, 1993  
A:Title: Purification, characterization, and cDNA cloning of an NADPH-cytochrome P450 reductase from mung bean  
A:Reference number: A47298; MUID:93219390; PMID:8464904  
A:Accession: A47298  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-690 <SHE>  
A:Experimental source: var. Berken, microsomes  
A:Note: sequence extracted from NCBI backbone (NCBIP:128723)  
C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase  
C:Keywords: flavoprotein; NADP; oxidoreductase  
F:82-689/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F:84-233/Domain: flavodoxin homology <FXD>

Query Match	13.2%	Score 723;	DB 2;	Length 690;
Best Local Similarity	30.6%;	Pred. No. 7.5e-33;		
Matches	191;	Conservative 109;	Mismatches 259;	Indels 66; Gaps 19;
Qy	477	AHNTPLLVLYGSMNGTAEGTARDLAD--IAMSXGFAPOVATLDSHAGN-----LPREG	527	
Db	77	AGTKTYTFGTGTGAEGFKAALAEIRKARYEKAAYKVVDLDDYDAADDLYEEKLUKES	136	
Qy	528	AVLIVTASY--NGHPPDNAKOFVDWLQASADE---VKGVRYSYFGCGDKNWAITYQKVA	583	
Db	137	LVFFMLATYGDGEPTDNAARFYKWFTEGDKERGIWLQKLTYGVEGLGNROY--SHFNKIGK	195	
Qy	584	FIDETLAAGAENIADRGEDASDDPEGTYVEERHMSDVAAYFNLDITENSEDNKSTLS	643	
Db	196	VWDEELAEQAQKRLVAVGLGDDQSDIEDDPSAMKSLWSELD-----QLLRDEDDANTVS	250	
Qy	644	LQFVDSAADM-----PLA-----KMHGAFSTNVVASKELQQQGSARS	680	
Db	251	TPYTAAILERYVVIHDPYTAASTYDNHSTVANGNTEFDIHHPCRVNVAVOKELHKPESDRS	310	
Qy	681	TRHLETLP--KEASYQGGHLYGVPYNYEGIVNRVYTFARGLDASQOIRLEAEKEKLAHL--	738	
Db	311	CIHLEFDISTSYTYDGHVGVYAENCNTEVETGKLLGQNLDFLFFSLHTDKDDGTSLG	370	
Qy	739	-----PLAKTVSYVE--ELLQTVLEQDPVTRTQLRAMAAKTVCPPHKVELEALLF---KQAY	789	
Db	371	GLSLPPPPGCSLRTALARYADLLNPRKAALLALATH--ASEPDSERLKLFLSPQCKDEY	429	
Qy	790	KEQVLAKRLTMLLELEKYPACEMKFFSEFT--ALLPSRTPRYYSISSSPRVDEKQASITVSU	848	
Db	430	SKWVYQSRLSEVMAEFTSAKPLPGVFFFAAIAPRLQPRYYSISSSPFAPQVRHVHTCAL	489	
Qy	849	VSGEAMSGYGEYKGIASNYL-----AELQEGTITCFISTPOSEFTLPKDPETPLIMVG	902	
Db	490	YVGTPPTG--RIHKGVCSTWKNALPSEKSDQSSAPIFIR--FSNFKLPVDHSIPILIMVG	546	
Qy	903	PGTGVAFFRGFVQARQOLKEQGQSLGEAHLYFCGRSPHEDYLYOEELNNAQSGIIT--LH	961	
Db	547	PGTGLAFFRGFLQERYALKEDGVQLGFPALLFFGCRNRQMDFIYEDELKSFVEQGSLELI	606	
Qy	962	TAFSRPNQPKTYVQHVMEQDGKKLTELDQGAHFVTCGDSGOMAPAVEATLMKSYADVH	1021	
Db	607	VAFSR--EGAEKEIVQHKMDKAHILWSLISQGGYLYVCGDAKMGARDVHRTLHSIVQEE	665	
Qy	1022	QVSEADARLWLQOLEEKGRYAKDVW	1046	
Db	666	NVDSTKAEAIYVKKLQMDGRYLRDWW	690	

RESULT 14  
T10720  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - opium poppy  
N: Alternate names: ferrihemoprotein p-450 reductase; NADP-cytochrome reductase  
C: Species: *Papaver somniferum* (Opium poppy)  
C: Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 03-Jun-2002

C;Accession: T10720  
C;R;Rosco, A.; Pauli, H.H.; Priesner, W.; Kutchan, T. M.  
Arch. Biochem. Biophys. 348, 369-377, 1997  
A;Title: Cloning and heterologous expression of NADPH-cytochrome P450 reductases from  
A;Reference number: Z17096; MUID:98096363; PMID:9434750  
A;Accession: T10720  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: mRNA  
A;Residues: 1-683 <ROS>  
A;Cross-references: EMBL:U67185; NID:G2580496; PIDN:AAC05021.1; PID:G2580497  
C;Function:  
C;Description: catalyzes the reduction of the heme-thiolate-dependent monooxygenases;  
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo  
C;Keywords: flavoprotein; NADP; oxidoreductase  
F;80-682/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F;82-230/Domain: flavodoxin homology <FX>

[illegible]

RESULT 15  
S37159  
NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - spring vetch  
C:Species: *Vicia sativa* (spring vetch, tare)  
C:Date: 20-May-1994 #sequence\_revision 03-Aug-1995 #text\_change 03-Jun-2002  
C:Accession: S37159  
R:Benveniste, I.: Beque-Kirn, C.: Lesot, A.: Hasenfratz, M.: Durst, F.

submitted to the EMBL Data Library, September 1993

A:Description: Isolation and characterization of a cDNA encoding an NADPH-cytochrome P450

A:Reference number: S37159

A:Accession: S37159

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-692 <BEN>

A:Cross-references: EMBL:226252; NID:g400531; PIDN:CAA81211.1; PID:g400532

C:Superfamily: NADPH-ferrithemoprotein reductase; flavodoxin homology; NADPH-ferrithemopro

C:Keywords: flavoprotein; NADP; oxidoreductase

F:83-691/Domain: NADPH-ferrithemoprotein reductase homology <FEH>

F:95-234/Domain: flavodoxin homology <FLX>

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Query Match      13.0%; Score 711; DB 2; Length 692;
Best Local Similarity 28.4%; Pred. No. 3.5e-32;
Matches 198; Conservative 120; Mismatches 287; Indels 92; Gaps 21;

QY 406 ALHEATLVLMKLFHDFEDHNYELDIKETLTPGEGFVVKAKSKKIPLGIGIPSPSTEQ 465
DB | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
32 ATTSAAVILGLV--FLMKSPDRSRELRPVTPK---FTVRKHEDDEV----- 76

QY 466 SAKVKRKAENAHNTPLLVLYGNSMGTAGTARDLAD--IAMSKGFAPQVATLDSHA--- 520
DB | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
77 -----DRGKTKVTVFYGTGTAGTAEKPAKALAEIKARYKAVKVVDMDDYVADD 126

QY 521 ----GNLPREGAVLIVTASY-NGHPPDNAQFVMDLQASADE---VKGVRYSVFCGDK 572
DB | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
127 DQVEEKLKRETLVFFMLATYGDGEPDINAARFVKWFTGEGKEGTWLQQLTYGVFALGNR 186

QY 573 NWATYYQKVPATIDETLAAGAENTADRGADASDDFEGTYEEHREHMSDVAAYFNLDI 632
DB | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
187 QY-EHFNKIGKIVDEDLTEQGAARLVPVGLGDDQSDIEDDFNAWKETLWPELD-----QL 240

QY 633 ENSDNKSTLSLQFVDSADMPILA-----KMHGAFSTNVVAS 669
DB | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
241 LRDEDDVNTASTPYTAASEYRVVHDPTVSPSYENHFNVANGGAVFDIHHPCRVNAVVR 300

QY 670 KELQPGSARSTRHLEIPL-KEASVQEGDHLGVIPRNYEGIVNRVTRFGLDASQQLRL 728
DB | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
301 RELHKPQSDRSCTHLEFDLSGTGVTVETGDHGVVAENCDETVEEAGKLLGQSLDLLFSL 360

QY 729 EAEKEKLAHL-----PLAKTVSVEELQ-VYELQDPVTRTQIRAMAATVCPPHKVELE 781
DB | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
361 HTDKEDGTSLGSLPFPFPGCTVTRTALACYADLLNPPRKAIVALAHAASEPSEAEERLK 420

QY 782 ALLE---KOAYKEQVLAKRLTLELLEKYPACEMKFSEFI-ALLPSIRPRYYSISSPRV 837
DB | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
421 FLSSPGKDEYSKWVGSORSLSLEVMAFPKAPPLGVFFAAIAPRLQPRYYSISSPRP 480

QY 838 DEKQASITVSVSGEAWSGYEGYKGIASNYLAEL-----QEGDTITCFISTPQSEFTLPKD 893
DB | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
481 APQRVHTCALVEGPTPTG-RIHKGVCSTWMSKATPLEKSHDCSRAPIFIRPSNFKLPAD 539

QY 894 PETPLMWGPGTGVQAPFRGCVQARKOLKEQOSLGEAHLYFCGRSPHEDLYQEELNAQ 953
DB | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
540 HSIPILMWGPGTGLAPFRGLQRLAKEDGVQLGALLFFGCRNRQMDFIYEDELNNEV 599

QY 954 SEGIIIT-LHTAFSRPNQPKTYVQHVMEQDGKKLIELLDQGAHFYTCGDSQMAPAVEAT 1012
DB | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
600 QQGAISELIVAFSR-EGPEKEYVQHKKMDKAEVLSLSIQGGYLYVCGDAKGMARDVHRS 658

QY 1013 LMKSYADVHQVSEAD---ARLWQOLEEKGRYAKDVW 1046
DB | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
659 L---HTIVQOQENADSSKAEATVKKLQMDGRYLWDV 692
```

Search completed: May 29, 2003, 08:31:43

Job time : 52 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 29, 2003, 08:22:51 ; Search time 26 Seconds  
(without alignments)  
1671.815 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 5457

Sequence: 1 TIKEMPQPKTFGELKNPL.....RLWLOLEKGRYAKDWAG 1048

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	5457	100.0	1048	1 CPXB_BACME	P14779 bacillus me
2	3314	60.7	1061	1 CYPD_BACSU	O08394 bacillus su
3	3281.5	60.1	1054	1 CYPE_BACSU	O08336 bacillus su
4	778.5	14.3	677	1 NCPR_MOUSE	P37040 mus musculu
5	777.5	14.2	677	1 NCPR_RAT	P00388 rattus norv
6	769	14.1	677	1 NCPR_PIG	P04175 sus scrofa
7	769	14.1	679	1 NCPR_RABIT	P00389 oryctolagus
8	767	14.1	676	1 NCPR_HUMAN	P16435 homo sapien
9	761.5	14.0	677	1 NCPR_CAVPO	P37039 cavia porce
10	735.5	13.5	671	1 NCPR_MUSDO	Q07994 musca domes
11	725.5	13.3	679	1 NCPR_DROME	Q27597 drosophila
12	723	13.2	601	1 NCPR_SALTR	P19618 salmo trutt
13	721	13.2	690	1 NCPR_PHAU	P37116 phaseolus a
14	702	12.9	714	1 NCPR_CATRO	Q05001 catharanthu
15	679.5	12.5	1147	1 NOS2_RAT	Q06518 rattus norv
16	679	12.4	1429	1 NOS1_MOUSE	Q92014 mus musculu
17	678	12.4	1429	1 NOS1_RAT	P29476 rattus norv
18	675	12.4	1434	1 NOS1_HUMAN	P29475 homo sapien
19	671.5	12.3	1147	1 NS2D_HUMAN	O60591 homo sapien
20	665.5	12.2	1144	1 NOS2_MOUSE	P29477 mus musculu
21	662	12.1	1435	1 NOS1_RABIT	O19132 oryctolagus
22	661	12.1	1153	1 NS2A_HUMAN	P35228 homo sapien
23	655	12.0	1136	1 NOS2_CHICK	Q90703 gallus gall
24	651.5	11.9	1149	1 NOS2_CAVPO	O54705 cavia porce
25	642	11.8	1174	1 NOS_RHOPR	Q26240 rhodnius pr
26	639	11.7	680	1 NCPR_CANMA	P50126 candida mal
27	614.5	11.3	1247	1 NOS_ANOST	O61608 anopheles s
28	608.5	11.2	1202	1 NOS3_HUMAN	P29474 homo sapien
29	602.5	11.0	1204	1 NOS3_BOVIN	P29473 bos taurus
30	594.5	10.9	1201	1 NOS3_MOUSE	P70313 mus musculu
31	590.5	10.8	1204	1 NOS3_PIG	Q28969 sus scrofa
32	587	10.8	680	1 NCPR_CANTR	P37201 candida tro
33	564.5	10.3	1350	1 NOS_DROME	Q27571 drosophila

#### RESULT 1

ID	CPXB_BACME	STANDARD	PRT	1048 AA
AC	P14779			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Bifunctional P-450:NADPH-P450 reductase (Cytochrome P450(BM-3))			
DE	(P450BM-3) [includes: Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase (EC 1.6.2.4)].			
GN	CYP102A1 OR CYP102			
OS	Bacillus megaterium.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1404;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=89291834; PubMed=2544578;			
RA	Ruettinger R.T., Wen L.-P., Fulco A.J.;			
RT	"Coding nucleotide, 5' regulatory, and deduced amino acid sequences of P-450BM-3, a single peptide cytochrome P-450:NADPH-P-450 reductase from Bacillus megaterium.";			
RL	J. Biol. Chem. 264:10987-10995(1989).			
RN	[2]			
RP	CHARACTERIZATION.			
RP	MEDLINE=92088245; PubMed=1727637;			
RA	Boddupalli S.S., Pramanik B.C., Slaughter C.A., Estabrook R.W., Peterson J.A.;			
RT	"Fatty acid monooxygenation by P450BM-3: product identification and proposed mechanisms for the sequential hydroxylation reactions.";			
RL	Arch. Biochem. Biophys. 292:20-28(1992).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-471.			
RP	MEDLINE=93342510; PubMed=8342039;			
RA	Ravichandran K.G., Boddupalli S.S., Hasemann C.A., Peterson J.A., Deisenhofer J.;			
RT	"Crystal structure of hemoprotein domain of P450BM-3, a prototype for microsomal P450 S.";			
RL	Science 261:731-736(1993).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-471.			
RP	MEDLINE=97185914; PubMed=9033595;			
RA	Li H.Y., Poulos T.L.;			
RT	"The structure of the cytochrome p450BM-3 haem domain complexed with the fatty acid substrate, palmitoleic acid.";			
RL	Nat. Struct. Biol. 4:140-146(1997).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (2.03 ANGSTROMS) OF 1-458 AND 459-649.			
RP	MEDLINE=99162523; PubMed=10051560;			
RA	Sevrioukova I.F., Li H., Zhang H., Peterson J.A., Poulos T.L.;			
RT	"Structure of a cytochrome P450-redox partner electron-transfer complex.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 96:18663-18668(1999).			
RN	[6]			
RP	X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS) OF 1-470.			
RP	MEDLINE=21552922; PubMed=11695892;			
RA	Haines D.C., Tomchick D.R., Machius M., Peterson J.A.;			

34	563	10.3	496	1	NOS2_RABIT	O19114 oryctolagus
35	537.5	9.8	678	1	NCPR_SCHPO	P36587 schizosacch
36	534.5	9.8	725	1	MTRR_HUMAN	O9ubk8 homo sapien
37	522	9.6	690	1	NCPR_YEAST	P16603 saccharomyc
38	518.5	9.5	598	1	CYSJ_ECOLI	P38038 escherichia
39	500.5	9.2	1153	1	NOS_DYMST	O61309 lymanaea sta
40	495.5	9.1	598	1	CYSJ_SALTY	P38039 salmonella
41	488.5	9.0	601	1	CYSJ_BUGAI	P57503 buchnera ap
42	480.5	8.8	919	1	NOS3_RAT	O62600 rattus norv
43	466.5	8.5	682	1	MTRR_CASEL	O17574 caenorhabdi
44	460	8.4	576	1	C972_SOYBN	O48921 glycine max
45	459.5	8.4	580	1	C973_ARATH	O23365 arabidopsis

#### ALIGNMENTS

RT "Pivotal role of water in the mechanism of P450BM-3.";  
 RL Biochemistry 40:13456-13465(2001).  
 CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. CATALYZES  
 CC HYDROXYLATION OF MEDIUM AND LONG-CHAIN FATTY ACIDS AT OMEGA-1,  
 CC OMEGA-2 AND OMEGA-3 POSITIONS, WITH OPTIMUM CHAIN LENGTHS OF 14-16  
 CC CARBONS (LAURIC, MYRISTIC, AND PALMITIC ACIDS). THE REDUCTASE  
 CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME  
 CC P450.  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
 CC ferrocyclochrome.  
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
 CC oxidized flavoprotein + H(2)O.  
 CC -1- COFACTOR: FAD AND FMN.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME  
 CC P450 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: J04832; AA87602.1; -  
 CC PIR: A34286; A34286.  
 CC DR PDB: 2HPD; 31-OCT-93.  
 CC DR PDB: 2BMH; 31-JUL-94.  
 CC DR PDB: 1FAG; 12-FEB-97.  
 CC DR PDB: 1FAH; 12-FEB-97.  
 CC DR PDB: 1B07; 23-SEP-98.  
 CC DR PDB: 1BVY; 23-FEB-99.  
 CC DR PDB: 1JPZ; 09-NOV-01.  
 CC DR InterPro: IPR001128; Cytochrome\_P450.  
 CC DR InterPro: IPR003097; FAD\_binding.  
 CC DR InterPro: IPR001709; FPN\_cyt\_redtase.  
 CC DR InterPro: IPR001226; Flavodoxin.  
 CC DR InterPro: IPR001433; Oxred\_FAD/NAD(P).  
 CC DR Pfam: PF00067; p450; 1.  
 CC DR Pfam: PF00175; NAD\_binding; 1.  
 CC DR Pfam: PF00258; flavodoxin; 1.  
 CC DR Pfam: PF00667; FAD\_binding; 1.  
 CC DR PRINTS: PR00371; FPNCR.  
 CC DR PRINTS: PR00385; P450.  
 CC DR PROSITE: PS00086; CYTOCHROME\_P450; 1.  
 CC KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
 KW Multifunctional enzyme; FMN; FAD; Flavoprotein; 3D-structure; NADP.  
 FT INIT\_MET 0 0  
 FT DOMAIN 1 471 CYTOCHROME P450.  
 FT DOMAIN 472 1048 NADPH-P-450 REDUCTASE.  
 FT BINDING 400 400 HEME.  
 FT TURN 12 13  
 FT TURN 15 16  
 FT TURN 17 20  
 FT HELIX 25 36  
 FT STRAND 39 44  
 FT STRAND 45 46  
 FT STRAND 47 52  
 FT TURN 55 61  
 FT TURN 62 62  
 FT TURN 64 66  
 FT STRAND 67 69  
 FT HELIX 73 82  
 FT TURN 83 84  
 FT HELIX 86 88  
 FT TURN 91 92  
 FT HELIX 94 107  
 FT TURN 109 111  
 FT HELIX 112 131  
 FT TURN 132 132  
 FT TURN 135 136  
 FT STRAND 139 140  
 FT HELIX 141 158

164 166  
 172 189  
 197 197  
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 361 362  
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 376 379  
 382 384  
 387 388  
 392 393  
 396 398  
 401 402  
 403 420  
 421 424  
 426 427  
 433 435  
 439 441  
 442 443  
 445 450  
 SQ SEQUENCE 1048 AA; 117650 MW; B55EB0DA599EAED5 CRC64;  
 Query Match 100.0%; Score 5457; DB 1; Length 1048;  
 Best Local Similarity 100.0%; Pred. No: 9e-298;  
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TIKEMPQPKTFGELKNLPLLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60  
 DB 1 TIKEMPQPKTFGELKNLPLLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60  
 QY 61 ACDESFDKNSQALKFVRDFAAGDGLFTSWTHEKNWKAHNNLLPSFSQAMKGYEAMV 120  
 DB 61 ACDESFDKNSQALKFVRDFAAGDGLFTSWTHEKNWKAHNNLLPSFSQAMKGYEAMV 120  
 QY 121 DIAVOLVQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNYRNSFYRDQPHPTTSMVRA 180  
 DB 121 DIAVOLVQKWERLNADHEIEVPEDMTRLTDLTIGLCGFNYRNSFYRDQPHPTTSMVRA 180  
 QY 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVNMNDLVKIIADRKASGEQSDLLTHMLNG 240  
 DB 181 LDEAMNKLQANPDDPAYDENKRFQEDIKVNMNDLVKIIADRKASGEQSDLLTHMLNG 240  
 QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAVLVD 300  
 DB 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLOKAAEAAVLVD 300  
 QY 301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGEVPLEKGDMLVLIPO 360  
 DB 301 PVPSYKQVKQLKYVGMVNLNEALRLWPTAPAFSLYAKEDTVLGEVPLEKGDMLVLIPO 360  
 QY 361 HRDKTIWGDVVEEFPREFENPSAIPQHAFKPFNGQQRACIGQQFALHATLVLGMMLKH 420  
 DB 361 HRDKTIWGDVVEEFPREFENPSAIPQHAFKPFNGQQRACIGQQFALHATLVLGMMLKH 420  
 QY 421 FDFEDHTNYELDIKETLTLLKPEGVFVVKAKSKIPGLGIPSPSTEQSAKVKRKAENHT 480  
 DB 421 FDFEDHTNYELDIKETLTLLKPEGVFVVKAKSKIPGLGIPSPSTEQSAKVKRKAENHT 480

Db 421 DFEDHTNYELDKETLTLKPEGVVAKSKKPLGGIPSPSTEQSAKKYKKAENAHT 480  
 QY 481 PLLVLYGNNMGTAEGTARDLADLAMSQFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540  
 Db 481 PLLVLYGNNMGTAEGTARDLADLAMSQFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540  
 QY 541 PDNAKQFVWLDAQSADDEVKGVRSVFGCGDKNWTYYQVPAFIDETLAAGAENIADR 600  
 Db 541 PDNAKQFVWLDAQSADDEVKGVRSVFGCGDKNWTYYQVPAFIDETLAAGAENIADR 600  
 QY 601 GEADASDDFGTVEWEHMHWSVAAAYFNLDIENSEDNKSTLSQFVDSADMPKAMHG 660  
 Db 601 GEADASDDFGTVEWEHMHWSVAAAYFNLDIENSEDNKSTLSQFVDSADMPKAMHG 660  
 QY 661 AFTSNVYASKELOQPGSARSTRHLEIPLKEASVQEGDHLGVIPRNYEGIVNVRTAREGL 720  
 Db 661 AFTSNVYASKELOQPGSARSTRHLEIPLKEASVQEGDHLGVIPRNYEGIVNVRTAREGL 720  
 QY 721 DASQIIRLEAEEKLAHLPLAKTVSVBELLYQVELQDPVTRTQLRAMAAKTVCPPHKVEL 780  
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 QY 841 QASITSVSWSGEAWSGYGYKGIASNYLAELQEGDITTCFTSPQSEFTLPLKDPETPLIM 900  
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 QY 901 VGPQTVAPRPGFVQARKQLKEQOSLGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 960  
 Db 901 VGPQTVAPRPGFVQARKQLKEQOSLGEAHLFGCRSPHEDYLYQBELENAQSEGIITL 960  
 QY 961 HTAFSRMPNPKTVQVHVMDQDKKLELDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 Db 961 HTAFSRMPNPKTVQVHVMDQDKKLELDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 QY 1021 HOVSEADARLWLQOLEEKGRYAKDVWAG 1048  
 Db 1021 HOVSEADARLWLQOLEEKGRYAKDVWAG 1048

## RESULT 2

CYPD\_BACSU STANDARD; PRT; 1061 AA.  
 AC 008394;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Probable bifunctional P-450:NADPH-P450 reductase 1 [includes:  
 DE Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase  
 DE (EC 1.6.2.4)].  
 GN CYPD OR CYP102A2.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=97453479; PubMed=9308178;  
 RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,  
 RA Duesterhoeft A., Ehrlich S.D.;  
 RT "Sequence of the Bacillus subtilis genome region in the vicinity of  
 RT the lev operon reveals two new extracytoplasmic function RNA  
 RT polymerase sigma factors SigV and SigZ.";  
 RL Microbiology 143:2939-2943(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., S.,  
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
 RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Rocha E., Roche M., Rose M., Sadate Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
 RA Tosato V., Uchiyama S., Vandebol M., Vannier F., Vassarotti A.,  
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,  
 RA Winters P., Wipac A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,  
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
 RT subtilis.";  
 RL Nature 390:249-256(1997).  
 CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE  
 CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME  
 CC P450 (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
 CC ferrocyclochrome.  
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
 CC oxidized flavoprotein + H(2)O.  
 CC -1- COFACTOR: FAD AND FMN (BY SIMILARITY).  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME  
 CC P450 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; D87979; BAA20123.1; -;  
 CC EMBL; Z99107; CAB12544.1; -;  
 CC HSSP; P14779; 1JPZ.  
 CC Subtilist; BG12871; cypD.  
 CC InterPro; IPR001128; Cytochrome\_P450.  
 CC InterPro; IPR003097; FAD\_binding.  
 CC InterPro; IPR001709; FPN\_cyt\_redctse.  
 CC InterPro; IPR001226; Flavodoxin.  
 CC InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 CC Pfam; PF00067; p450; 1.  
 CC Pfam; PF00175; NAD\_binding; 1.  
 CC Pfam; PF00258; flavodoxin; 1.  
 CC Pfam; PF00667; FAD\_binding; 1.  
 CC PRINTS; PR00371; FPNCR.  
 CC PRINTS; PR00385; P450.  
 CC PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 CC Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
 KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;  
 KW Complete proteome.  
 KW DOMAIN 1 474 CYTOCHROME P450.  
 FT DOMAIN 475 1061 NADPH-P-450 REDUCTASE.  
 FT BINDING 403 403 HEME (BY SIMILARITY).  
 SQ SEQUENCE 1061 AA; 119467 MW; 7915DACC20578978 CRC64;

Query Match

60.7%; Score 3314; DB 1; Length 1061;

Best Local Similarity 59.5%; Pred. No. 7.1e-178;

Matches 628; Conservative 156; Mismatches 259; Indels 12; Gaps 6;

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QY 7 IPOKTFGLGNLPLDKDKPTLSLKLAEQGPFOIHTPAGTTIVVSGHVLKEVCDE 66
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 SREDKNLSQALKFVRDFAGDGLFTSWTHEKNWKAHNLPSFSQAMGYHAMVDIAV 124
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 67 ERFDKSIEGALKVRAFSGDGLFTSWTHEPNWKAHNLMPFESQAMKDYHEKWDIAV 126
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 125 QLVQKWERLNADHIEVPEDMTRLTDTGLCGFNFRFNSFYQDQPHPFITSMVRALDEA 184
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QY 127 QLIQKWARLNPNPAVDVPGDMTRLTDTGLCGFNFRFNSFYQDQPHPFITSMVRALDEA 186
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 247 ETGEPLDENIRYQIITFLIAGHETTSGLLSFALYLVKNPNHVLQKAAEAAAVLVDVPP 306
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QY 307 TYQVQVLELYIRMLNESLRLMPTAPAFSLYKEDTVLGEYPLEKGDMLVLPOLHRD 366
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 367 RDWAGKDAEERFEREHQDQVPHAYKFGNGORACIGQOPALHEATLVGLMNLKHEDF 426
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 424 EDHNTYELDIKEFLTLKPGFVVKAKSKIPLGGIPSPTEQSA---KKVRKAENA--- 477
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QY 427 IDHENYELDIKOTLTKPGDFHISVQSRHQEAHADVQAAKAAPEQKEKTEAKGASVI 486
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 478 --HNTPLLVLYGSMCTAGTADLADIAWSGFAPOVATLDSHAGNLREGAVLVTAS 535
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 487 GLNRPFLVLYGSDTAGVARELADTASLHGVRRTKAPLNDRIKLRGKAVLVTSS 546
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QY 536 YNGHPDPAQFQVWLDQASADSVKGVRYSVFCGDKNWTATYQKVPFIDETLAAGAE 595
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 547 YNGKPPSNAGQFQVWLDQASADSVKGVRYSVFCGDKNWTATYQKVPFIDETLAAGAE 606
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 596 NIADREASDADFEGTYEWEHMSDVAANFLNDI-ENSEDNKTLISLQFVDSAADMP 654
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 607 RFSARGEGDVSGDFEGDQWELKSMWADAIAKAFGLNENADKERSTLSLQFVGLGESP 666
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 655 LAKMHGAFSTNVVAKELQPGSARSTRHLELTPKEASYQEGDHLGVIPRYEGVNVSR 714
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 727 LHRFLGKGTQVTLSSAGRSAGHLPLGRPVSLDHLSSYSVEVQEAATRAQIRELASFTVC 786
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 774 PHKVELEALLEKQAYKEQVLAQLRLTMELEKYPACEMKFSEFIALLSIRPRYSISS 833
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 787 PPHRELELSAEGVYQEQILKRIKRIKRIKRIKRIKRIKRIKRIKRIKRIKRIKRIKRI 846
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 954 SEGITLTHAFGRMPNQPTYYVQHVMEQDKKLIELLDQGAHYICGDSQMAPAVEATL 1013
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 1026 QKAYQAVHGTGEQEAQNWLRLHLODTGMYAKDVWAG 1060
RESULT 3
CYPE_BACSU STANDARD; PRT; 1054 AA.
AC 008336;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable bifunctional P-450:NADPH-P450 reductase 2 [Includes:
DE Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
DE (EC 1.6.2.4)]
GN CYPE OR CYP102A3.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97453479; PubMed=9308178;
RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
RA Dusterhoeft A., Ehrlich S.D.;
RT "Sequence of the Bacillus subtilis genome region in the vicinity of
RT the lev operon reveals two new extracytoplasmic function RNA
RT polymerase sigma factors Sigv and Sigz."
RL Microbiology 143:2939-2943(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Chouliet S., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denicot F., Devine K.M., Dusterhoeft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
RA Ghim S.I., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Yamakoshi A., Tanaka T., Terstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
CC P450 (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferrocyclochrome.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- COFACTOR: FAD AND FMN (BY SIMILARITY).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
CC P450 FAMILY.
CC -----
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; U93874; AAB80867.1; -;  
 DR EMBL; Z99117; CAB14658.1; -;  
 DR HSSP; P14779; LJPZ.  
 DR Subtilist; BG12299; cypE.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR InterPro; IPR003097; FAD\_binding.  
 DR InterPro; IPR001709; FPN\_cyt\_redctse.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00067; P450; 1.  
 DR Pfam; PF00175; NAD\_binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR PRINTS; PR00371; FPNCR.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
 KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;  
 KW Complete proteome.  
 FT DOMAIN 1 475 CYTOCHROME P450.  
 FT BINDING 472 1053 NADPH-P-450 REDUCTASE.  
 FT BINDING 403 403 HEME (BY SIMILARITY).  
 SQ SEQUENCE 1054 AA; 118675 MW; 705F8E27866CALLE CRC64;

Query Match 60.1%; Score 3281.5; DB 1; Length 1054;  
 Best Local Similarity 58.5%; Pred. No. 4.6e-176;  
 Matches 614; Conservative 173; Mismatches 254; Indels 9; Gaps 6;

QY 5 MPQPKTGEKLNPLNTRDQVQALMKIADBLGIFKEAPGRVTRVLSORLKEACDE 64  
 DB 7 IPQPKTGLPLNPLEKEQLSQSLRWIADBLGIFRDFEGSVSVFSGHNLVAECDE 66  
 QY 65 SRFDKNIQALKFVYDFAGDGLFTSWTHEKNWKAHNLPLSFQQAQMGVHAMVVDIAV 124  
 DB 67 KRFDKNLGKLGKQVREGGDGLFTSWTHEPNWKAHNLPLSFQQAQMGVHAMVVDIAV 126  
 QY 125 QLVQKWERLNADERIEVPEDTRTLDTIGLCGFNYRFSFYRQPHPIFITSVMRALDEA 184  
 DB 127 QLVQKWERLNADERIEVPEDTRTLDTIGLCGFNYRFSFYRQPHPIFITSVMRALDEA 186  
 QY 185 MNKLQANPDPAVDENKRFQEDIKVNDLVKIIADKASGEQS-DLLTHMLNGKDP 243  
 DB 187 MNQSKRLGLQDKMVKTKLQFQKDIYMNLSVDRMIAERKANPDENKDLLSLMLYAKDP 246  
 QY 244 ETGEPDLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAARVLPVP 303  
 DB 247 VTGETLDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEAARVLPVP 306  
 QY 304 SYKQVKQLKGYVMVNEALRLWTPAPAFSLYAKEDTVLGGEPYKDELMLVLPQLHRD 363  
 DB 307 EYKQIQQLKRYMVLNETRLYPAPAFSLYAKEDTVLGGEPYKDELMLVLPQLHRD 366  
 QY 364 KTINGDDVEERPRPFENPSAIPQAFKPGNGQACIGQFALHEATVLMGLMKHFD 423  
 DB 367 QNAGWDPAEDPRPFEDPSSIPHHAYKPGNGQACIGQFALHEATVLMGLMKHFD 426  
 QY 424 EDHNYELDIKETITLKEGPPVKAQSKKIPGLGIPSPSTBQS---AKKVRKKAENAHNT 480  
 DB 427 INHGYELKIEALITPDDPKITVTKPRK--TAAINVQRKQADIKATKPKPKPHGT 484  
 QY 481 PLLVLYGSMGTAGCTARDLADIAMSKGFAPOVATLDSHAGNLPREGAVLITVTSYNGHP 540  
 DB 485 PLLVLYGSMGTAGCTARDLADIAMSKGFAPOVATLDSHAGNLPREGAVLITVTSYNGHP 544  
 QY 541 PDNAKQFVDWLDQASADEVKGVRSVFEGCGDKNWATTYQKVPAPFIDETLAAGAENIADR 600

DB 545 PDNAAGFVWLKEEGOLKGVYAVFCGNGRWSASTYQIRPLRIDDMKAKGASRLTAI 604  
 QY 601 GEADASDDFCTYEEMREHMSDVAAYENLDIENSEDNKSTLSLQFVDSADMLAKMHG 660  
 DB 605 GEGDAADDFFESHRESWENRFWKETMDAFDIMEIAQKEDRPSLITFLSETETPVAKAYG 664  
 QY 661 AFSTNVYASKLQPGSARSSTRHLEIELPKEASQEGDHLGVIPRNYEGIVNRYTAREGL 720  
 DB 665 AFEGLVLENRELQTAASTRSTRHLEIEIPACKTYKEGDHIGILPKNSRELQVLSRGL 724  
 QY 721 DASQIRLEAEEKLAHLPLAKTVSVELL--QYVELQDPVTRTQLRAMAATVCPPHKVE 779  
 DB 725 QSNHVIKVGSAH--MAHLPMDRPIKVVDLLSSYVELQEPASRLQRLASTVCPPHQKE 783  
 QY 780 LEALLEKQA--YKEOVLAKRLLMLELKYKACEKMFSEFIALLSIRPRYSISSSPVD 838  
 DB 784 LEQLVSDGTYKEQLAKRLTMDLFEDYPACEMPFERFLALLSLKPRYSISSSPKVH 843  
 QY 839 EKQASITVSVVSGEAWSGYGEYKGTASNYLAELQEGDTITCFSTPQSEFTLPKDPETPL 898  
 DB 844 ANIVSMIVGVVKSASWSGRGEYGVASNYLAELTGDAAACFIRTPQSGFQMPNDPETPM 903  
 QY 899 IMVPGTGAVPFRGFVQARKOLKEGQSLGSAHLYFGCRSHEDLYOELENAQSEGI 958  
 DB 904 IMVPGTGAVPFRGFVQARKOLKEGQSLGSAHLYFGCRSHEDLYOELENAQSEGI 963  
 QY 959 TLHTAFSRPNQPTVQVHVMQDGKLLIEDLQGAHYICGDSQSOMAPAVEATLMSKYA 1018  
 DB 964 TIRRCYSRVNEPKGYVQHLKQDTQKLTUETGAHYICGDSQSOMAPADVERTLRLAYE 1023  
 QY 1019 DVHGVSEADARLQLQLEEKGRYARDVWAG 1048  
 DB 1024 AEKASQESAVWLQKLDQRRYKVDWVG 1053  
 RESULT 4  
 NCPR\_MOUSE  
 ID NCPR\_MOUSE STANDARD; PRT; 677 AA.  
 AC P37040;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ddy;  
 RX MEDLINE=94281246; PubMed=8011664;  
 RA Ohgaya S., Ishizaki K., Kamataki T., Shinriki N.;  
 RT "Mouse NADPH-cytochrome P-450 oxidoreductase: molecular cloning and  
 functional expression in yeast."  
 RL Biochim. Biophys. Acta 1186:137-141(1994).  
 CC -!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
 TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
 TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
 CC -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
 ferrocycytochrome.  
 CC -!- COFACTOR: FAD AND FMN.  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE  
 ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
 CC -!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
 FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
 NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
 REDUCTASE.  
 CC -----  
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EMBL: DJ7571; BAA04496.1; -.  
HSSP; P00388; 1AM0.  
SWISS-2DPAGE; P37040; MOUSE.  
MGI: 97744; Por.  
InterPro: IPR003097; FAD\_binding.  
InterPro: IPR001709; FPN\_cy\_redutsee.  
InterPro: IPR001094; Flavodoxin\_like.  
InterPro: IPR001226; Flavodoxin.  
InterPro: IPR001433; Oxred\_FAD/NAD(P).  
Pfam: PF00175; NAD\_binding; 1.  
Pfam: PF00258; flavodoxin; 1.  
Pfam: PF00667; FAD\_binding; 1.  
PRINTS; PR00369; FLAVODOXIN.  
PRINTS; PR00371; FPNCR.  
KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
KW Membrane; Acetylation.  
FT INIT\_MET 0  
FT MOD\_RES 1 0 BY SIMILARITY  
FT NP\_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
FT NP\_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).  
FT NP\_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).  
FT NP\_BIND 529 547 NADP (RIBOSE PART) (BY SIMILARITY).  
FT NP\_BIND 624 640 NADP (ADP PART) (BY SIMILARITY).  
SQ SEQUENCE 677 AA; 75912 MW; 0065C14D0E1C5EF8 CRC64;  
Query Match 14.3%; Score 778.5; DB 1; Length 677;  
Best local similarity 32.3%; Pred. No. 2.6e-36;  
Matches 212; Conservative 106; Mismatches 267; Indels 71; Gaps 22;  
444 FVVKASKKIP---LGGIPSPSTEQS-AKKYKKAENAHNTPLLVLYGNSMGTAGTAR 498  
41 FIFKKEEIPESKIQTTAPPVGSFVEKMKKTGRN-----IIVFGSGQTGAEEFAN 95  
499 DLADIAMSGFAPOVATLDSH-----AGNLP--EGAVLIWTASY-NGHPPDNAKQFVWL 551  
96 RLSDAHRYGMRGMSADPEYDLADLSLPEIDKSLVFCMATYTGSGDPTDNAQDFYDWL 155  
552 DQASADEVGVRYVFGCGKNWATYQKVA---FIDETLAAGKNAIDRGEADASDD 608  
156 QETDVD-LGCVKFAVFLGK-----TYEHFNAMGKYVDQLEQLGAQRIFELGLGDDGN 210  
609 FEGTYEWEHMSDVAAYENLDIENSNDKSTLSLQFVDSADMDPLAKMH----- 659  
211 LEEDFITWREQWPAVCEFFGVEATGEESIRQYELVWHE---DMDTAKVYTGEMGRLS 267  
660 -----GAFSTNVVASKELQPGSARSSTRHLEIEL-PKEASYQEGDHLGVIPRNY 707  
268 YENQKPPDKAPNPLAAVTTNRKLQ-GYERHLMHLELIDSDSKIRYESGDHVAVYPAND 326  
708 EGLNVRTARFG--LDASQOIRLEAEEKLAHLPLAKTVSVBELLOYVELQDPVTRQLR 765  
327 STLVNIGILGADLVIMSLNLDSENNKHPFPCPTTYRTALTYLDTNP-PRTNVL 385  
766 AMAAKVCPVP-----HKVELKALKEQAYKQVLAKRLTLMLELEKYPACEMKTFEFTA 819  
386 YELAQVAPSPSQEHUHKMASSSGEGKELYLSWVVEARRHILAILQDYPSLRPPDHICE 445  
820 LLPISIRPRYSISSSPVDEKQASTIVSVVSGEAMSGYGEYKGIASNYL-----AELOE 873  
446 LLPRLQARYYSIASSSKVHPNSVHICAVAVEYEAKSGRYN-KGVATSWLRKTEPAGENG 504  
874 GDTITCFISTPQSEFTLPKDPETPLMWGPGTGVAPFRGVQARKOLKQSGSLGAHLY 933  
505 RALVPMFVR--KSQFLPLPKFTPTVIMVGGTGVAPFMGFIQERAWLRQEGVGETLTY 562  
934 FGRSPHEDLYQEELENAQSEGIT-LHTAFSRMNPQKTVQVHVMEDGKKLIELLDQ 992  
563 YGCRSDDELYLREELARFKDQALTQLVNATSR-EQAHKVVYVQHLLAKDKKHLKLIHE 621

993 -GAHFVIGDGSOMAPVATLTKMSYADVHVQSEADARLWLOOLEKGRYAKDVWA 1047  
622 GGAHYVCGDARNMAKDVONTFYDVAEFGPMEHTQAVDYVVKLTKGKRYSLDWS 677  
RESULT 5  
NCPR\_RAT  
ID NCPR\_RAT STANDARD; PRT; 677 AA.  
AC P00388;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).  
GN POR.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85140278; PubMed=3919392;  
RA Porter T.D.; Kasper C.B.;  
RT "Coding nucleotide sequence of rat NADPH-cytochrome P-450  
oxido-reductase cDNA and identification of flavin-binding domains.";  
Proc. Natl. Acad. Sci. U.S.A. 82:973-977(1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86163762; PubMed=3082610;  
RA Murakami H.; Yabusaki Y.; Ohkawa H.;  
RT "Expression of rat NADPH-cytochrome P-450 reductase cDNA in  
Saccharomyces cerevisiae.";  
DNA 5:1-10(1986).  
RN [3]  
RP SEQUENCE OF 413-677 FROM N.A.  
RC STRAIN=Wistar; TISSUE=Liver;  
RX MEDLINE=91104888; PubMed=2125483;  
RA Porter T.D.; Beck T.W.; Kasper C.B.;  
RT "NADPH-cytochrome P-450 oxidoreductase gene organization correlates  
with structural domains of the protein.";  
Biochemistry 29:9814-9818(1990).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
RX MEDLINE=97385116; PubMed=9237990;  
RA Wang M.; Roberts D.L.; Paschke R.; Shea T.M.; Masters B.S.S.;  
Kim J.-J.P.;  
RT "Three-dimensional structure of NADPH-cytochrome P450 reductase:  
prototype for FMN- and FAD-containing enzymes.";  
Proc. Natl. Acad. Sci. U.S.A. 94:8411-8416(1997).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (1.80 ANGSTROMS) OF MUTANTS.  
RX MEDLINE=21369908; PubMed=11371558;  
RA Hubbard P.A.; Shen A.L.; Paschke R.; Kasper C.B.; Kim J.-J.P.;  
RT "NADPH-cytochrome P450 oxidoreductase. Structural basis for hydride  
and electron transfer.";  
J. Biol. Chem. 276:29163-29170(2001).  
CC -!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
CC -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2  
ferricytochrome.  
CC -!- COFACTOR: FAD AND FMN.  
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
CC -!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
REDUCTASE.  
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DR InterPro: IPR001709; FPN\_cyt\_redtse.  
DR InterPro: IPR001094; Flavodoxin\_like.  
DR InterPro: IPR001226; Flavodoxin.  
DR InterPro: IPR001433; Oxred\_FAD/NAD(P).  
DR Pfam: PF00175; NAD\_binding; 1.  
DR Pfam: PF00258; flavodoxin; 1.  
DR Pfam: PF00667; FAD\_binding; 1.  
DR PRINTS; PR00369; FLAVODOXIN.  
DR PRINTS; PR00371; FPNCR.  
KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
KW Membrane; Acetylation.  
FT INIT\_MET 0  
FT MOD\_RES 0  
FT NP\_BIND 169 200 ACETYLATION (BY SIMILARITY).  
FT NP\_BIND 313 324 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
FT NP\_BIND 450 460 FAD (ADP PART) (BY SIMILARITY).  
FT NP\_BIND 528 546 FAD (FLAVIN PART) (BY SIMILARITY).  
FT NP\_BIND 623 639 NADP (RIBOSE PART) (BY SIMILARITY).  
FT NP\_BIND 639 659 NADP (ADP PART) (BY SIMILARITY).  
FT CONFLICT 54 54 S -> T (IN REF. 2).  
FT CONFLICT 163 163 T -> S (IN REF. 2).  
FT CONFLICT 174 174 T -> D (IN REF. 3).  
FT CONFLICT 339 339 T -> A (IN REF. 3).  
FT CONFLICT 378 378 N -> D (IN REF. 3).  
FT CONFLICT 400 400 Q -> E (IN REF. 3).  
FT CONFLICT 446 446 R -> L (IN REF. 2).  
FT CONFLICT 502 502 N -> D (IN REF. 3).  
FT CONFLICT 508 508 V -> L (IN REF. 2 AND 3).  
FT CONFLICT 674 674 D -> N (IN REF. 3).  
SQ SEQUENCE 677 AA; 76701 MW; 26073A0B97EE3DFF CRC64;  
Query Match 14.1%; Score 769; DB 1; Length 677;  
Best Local Similarity 31.9%; Pred. No. 8.9e-36;  
Matches 224; Conservative 109; Mismatches 275; Indels 94; Gaps 27;  
QY 401 IGQFALHEAT-----LVLGMLKHFEDEHTNY--ELDIKETLT--LKPGFVVVKA 450  
DB 15 VAEESLFATDMVFLSLVGLTTFIFPKKKDEVPEFSKETITSSVKDSFV----- 69  
QY 451 KKIPGLGIPSTEQSAKKVRKKAENAHNTPLLVYGSNMGTAEGTARDLADIAKSGFA 510  
DB 70 -----ERKKKTGRN-----LIIVFGSQTGTAEFAFNLSKDAHYGNR 107  
QY 511 PQVATLD-----SHAGNLP-EGAVLI-VTASY-NGHPDPAKOFVDWLQASADEVKYR 563  
DB 108 GMAADPEEYDLSDLSLPIENALAVFCMATYCEGDPDQAQDFYDMLQEAQVDV-LTG 166  
QY 564 YSVEGCGKNWATTYQKPA---FIDETLAAGAENIADRGADASDDPEGTYEWEH 620  
DB 167 YAVFGLGNK-----TYEHFNAGKYVDKRLQEQAGRIQFGLGLGDDGNLEEDFITW 222  
QY 621 WSDVAAYFNLDIENSNDKSTLSLQF---VDSAA-----DMLAKMHGAFS 663  
DB 223 WPAVCEHFGVEATGEBSIRQYELVHTDMDTAVVYTGEMGRKSVENQKPPFDKKNPL 282  
QY 664 TNVASKELQPGSGARSTRHEIEL-PKEASQEGDHLGIVIPNVEGIVNVRTARGLDA 722  
DB 283 AVVTTNRKLNQ-GTERHLMHLELDISDSIRYESGDHVAVPANDSALVNQLGELTIDL 341  
QY 723 SQQI---RLEAREEKLAHLPLAKTSVVELLYQVLOQDPTVTRLMAAKTVCPPHKVE 779  
DB 342 DIVMSLNLDSESNRHPPECTTYRT-ALTYLDITNPPRRNVLYELAQYASEPSEQ 400  
QY 780 LEALLE-----KOAYKEQYLAKLTMLELLEKYPACEMKFSFIALLPISIRPYYSISS 834  
DB 401 LRKMASSGEGELYLSWVVEARRHILAIQDYPSLRPPIDHLCERLPLOQARYSIASS 460  
QY 835 PVYDEKQASITVSVSGEANSYGEGYKIASNYL-AELQEGT-----ITCISTPQSEF 888  
DB 461 SKVHPNSHICAVVVEYETKSGRVN-KGVATSWLRAKEPAGNGRRALVPMEVR--K 517  
QY 889 TLPKDPTPLIMVGPGTGVAPRFGFOARKQLKEQSGISGEAHLVFGCRSPHEDYLQEE 948  
DB 518 RLFPKATTPVIMVGPGTGVAPFIFGIQERAWLQEQGKEVGETPFLLYGCCRDEEDYL 977

QY 949 LENAOSGIIIT-LHTAFSRPNOP-KTYVQHVMEODGKKLIELL-DOGAHFYICGDSOM 1005  
DB 578 LAQFRAKGAITRLSVAFSR--EQPKVYVQHLLKRDKEHLKHLIDGGHAIYICGARNM 635  
QY 1006 APAVEATLMKSYADHVQVSEADARLWLOOLEEKGRYAKDVWA 1047  
DB 636 ARDVQNTFCDIVAEQGPMEHAQAVDYVKKLMTKGRYSLDWS 677

## RESULT 7

NCPR\_RABBIT  
ID NCPR\_RABBIT STANDARD; PRT; 679 AA.  
AC P00389;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).  
GN POR.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_Taxid:9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=87137361; PubMed=3029050;  
RA Katagiri M., Murakami H., Yabusaki Y., Sugiyama T., Okamoto M.,  
RA Yamano T., Ohkawa H.;  
RT "Molecular cloning and sequence analysis of full-length cDNA for  
RT rabbit liver NADPH-cytochrome P-450 reductase mRNA.";  
RL J. Biochem. 100:945-954 (1986).  
RN [2]  
RP PARTIAL SEQUENCE OF 1-81.  
RC TISSUE=Liver;  
RX MEDLINE=82167456; PubMed=6802823;  
RA Black S.D., Coon M.J.;  
RT "Structural features of liver microsomal NADPH-cytochrome P-450  
RT reductase. Hydrophobic domain, hydrophilic domain, and connecting  
RT region.";  
RL J. Biol. Chem. 257:5929-5938 (1982).  
CC -!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
CC -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
CC ferrocycytochrome.  
CC -!- COFACTOR: FAD AND FMN.  
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
CC -!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
CC REDUCTASE.  
CC  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: D00101; BAA00063.1; -  
CC EMBL: X04610; CAA28279.1; -  
CC PIR: A25505; A25505.  
CC PIR: A05233; A05233.  
CC HSP: P16435; LBIC.  
CC InterPro: IPR003097; FAD\_binding.  
CC InterPro: IPR001709; FPN\_cyt\_redtse.  
CC InterPro: IPR001094; Flavodoxin\_like.  
CC InterPro: IPR001226; Flavodoxin.  
CC InterPro: IPR001433; Oxred\_FAD/NAD(P).  
CC Pfam: PF00175; NAD\_binding; 1.



DR Pfam; PF00258; flavodoxin; 1.  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; PFNCR.  
 KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
 KW Membrane; Acetylation.  
 FT MOD\_RES 72 72 ACETYLATION.  
 FT NP\_BIND 171 202 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 315 326 FAD (ADP PART) (BY SIMILARITY).  
 FT NP\_BIND 452 462 FAD (FLAVIN PART) (BY SIMILARITY).  
 FT NP\_BIND 530 548 NADP (RIBOSE PART) (BY SIMILARITY).  
 FT NP\_BIND 625 641 NADP (ADP PART) (BY SIMILARITY).  
 FT CONFLICT 40 41 YW -> NY (IN REF. 2).  
 FT CONFLICT 53 53 E -> N (IN REF. 2).  
 SQ SEQUENCE 679 AA; B1A163FA53A5988B CRC64;  
 Query Match 14.1%; Score 769; DB 1; Length 679;  
 Best Local Similarity 31.7%; Pred. No. 8.9e-36;  
 Matches 212; Conservative 111; Mismatches 250; Indels 96; Gaps 24;  
 QY 444 FVYKAKSKKIP----LGIPSPSTEQA--KVKRKAENAHTPLLVLYSGNMGTA 497  
 DB 42 FLFRKKKEEYDEFTKIQAPTSVSSVKESSEFVEKMKKTGRN-----IVFYGSQTAEFA 96  
 QY 498 RLADITAMSGFAPQVATLDH-----AGNLPREGAVLIV--TASY-NGHPPDNAKQFVDW 550  
 DB 97 NRLSKDAHRYGMRGMAADPEYDLADLSLPEINNALAVFCMATYGGEDPTDNAQDFYD 156  
 QY 551 LQASADEVGVSYVFGCGDKNWTYQKVA---FIDETLAAGAENADTAGEADSD 607  
 DB 157 LQETDVD--LSGVAVFGLNK-----TYEHFNAMGYVDORLQGLGQRIEFGMGDDDA 211  
 QY 608 DFEGTYEWEHMSVDAVYFNLDIENSEDNKSTLSLQFYDVSADMPAKMH-----659  
 DB 212 NLEEDFTWREQFWPACVCFHVEATGEESIRQYELVL---HTDIDVAKVYQGMGRK 268  
 QY 660 -----GAFSTNVVASLQOPGASRSTRHLEIEL-PKEASYQSGDHLGVIPRN 706  
 DB 269 SYENQKPPDAKPFATVTTNRKLNQ-GTERHLMHLELDISDSKIRYESGDHVVYPAN 327  
 QY 707 YEGIVNVTARFGLDASQOI---RLAEAEKLAHLPL-----AKTVSV 746  
 DB 328 DSALVNLGELIGADLDVMSLNNLDESNKHPFCPTSYRTALTYILDTNPPRNVL 387  
 QY 747 EELQVVELQDPVTRTOLRAMAKTYCVPKPKVELEALLEKQAYKEQVLAKRMLMLELLEK 806  
 DB 388 YELAQA--ADPAEQEQLRWKSSSG-----EGKELYLSWVVEARRHILAILQD 434  
 QY 807 YPACEMKFSEFIALLPSIRPYYSISSPRVDEKQASITVSVSGEAWSGYGEYKGTASN 866  
 DB 435 YPSLRPPIDHLCLELPRLQARYYSIASSSKVPNSVHICAVAVEYETKAGRLN-KGVATS 493  
 QY 867 YL-AELQEGDT-----ITCFISVQSEFTLPKDPETPLIMVPGCTGVAPRFGVQARKQL 920  
 DB 494 WLRAKEPAGNGRGLVPMFVR--KSQFLRPFKATTPVIMVPGCTGVAPRFGVQARKQL 551  
 QY 921 KEQGSGLGEAHLFGCRSPHEDYLYQEELENAQSEGIIT-LHTAFSGMNPQKTYGVHM 979  
 DB 552 RQCGKEVGETLLYGCRRAAEDYLYRELAGFKDGTLSQLNVAFSREQAQ-KVYVQHLL 610  
 QY 980 EQDGKLIELLDQ-GAHFYTCGGGSMAPAVEATLMKSYADVHQVSPADARLMQLQLEEK 1038  
 DB 611 RDKHEHLWRLIHGGAHIYVCGDARNARDVQNTFYDIVAELGAMAHAQAVDVYVKLMTK 670  
 QY 1039 GRVAKDYWA 1047  
 DB 671 GRVSLDWS 679

RESULT 8

NCPR\_HUMAN

ID NCPR\_HUMAN STANDARD; PRT; 676 AA.

AC P16435; Q16455; Q9H3M8;

DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).  
 GN POR OR CIPOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=90105390; PubMed=2513880;  
 RA Haniu M., McManus M.E., Birkett D.J., Lee T.D., Shively J.E.;  
 RT "Structural and functional analysis of NADPH-cytochrome P-450  
 RT reductase from human liver: complete sequence of human enzyme and  
 RT NADPH-binding sites.";  
 RL Biochemistry 28:8639-8645(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92198003; PubMed=1550342;  
 RA Shephard E.A., Palmer C.N., Segall H.J., Phillips I.R.;  
 RT "Quantification of cytochrome P450 reductase gene expression in human  
 RT tissues.";  
 RL Arch. Biochem. Biophys. 294:168-172(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Czerwinski M., Sahni M., Madan A., Parkinson A.;  
 RT "Polymorphism of human CYPOR: expression of new allele.";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Murakami H.O., Ogawa H., Nishimoto Y.;  
 RT "cDNA cloning and characterization of NADPH-cytochrome P-450 reductase  
 RT in human HL-60 cell.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 61-241.  
 RX MEDLINE=99156068; PubMed=10048323;  
 RA Zhao Q., Modi S., Smith G., Paine M., McDonagh P.D., Wolf C.R.,  
 RA Tew D., Lian L.Y., Roberts G.C., Driessen H.P.;  
 RT "Crystal structure of the FMN-binding domain of human cytochrome P450  
 RT reductase at 1.93 A resolution.";  
 RL Protein Sci. 8:298-306(1999).  
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
 CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome -> NADP(+) + 2  
 CC ferriocytochrome.  
 CC -1- COFACTOR: FAD AND FMN.  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE  
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
 CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
 CC REDUCTASE.  
 CC -----  
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 CC -----  
 CC EMBL; S90469; AAB21814.1; -  
 CC EMBL; AF258341; AAG09798.1; -  
 CC EMBL; AB051763; BAB18572.1; -  
 CC PIR; A33421; A33421  
 CC PDB; 1B1C; 24-NOV-99.  
 CC Genew; HGNC:9208; POR.  
 CC MIM; 124015; -

DR InterPro: IPR003097; FAD\_binding.  
DR InterPro: IPR001709; FPN\_cyt\_redtse.  
DR InterPro: IPR001094; Flavodoxin\_like.  
DR InterPro: IPR001226; Flavodoxin.  
DR InterPro: IPR001433; Oxred\_FAD/NAD(P).  
DR Pfam: PF00175; NAD\_binding; 1.  
DR Pfam: PF00258; flavodoxin; 1.  
DR Pfam: PF00667; FAD\_binding; 1.  
DR PRINTS: PR00369; FLAVODOXIN.  
DR PRINTS: PR00371; FPNCR.  
KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
KW Membrane; Acetylation; Polymorphism; 3D-structure.  
FT INIT\_MET 0  
FT MOD\_RES 1  
FT NP\_BIND 169 200 FWN (PYRIMIDINE PART) (BY SIMILARITY).  
FT NP\_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).  
FT NP\_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).  
FT NP\_BIND 528 546 NADP (RIBOSE PART) (BY SIMILARITY).  
FT NP\_BIND 622 638 NADP (ADP PART) (BY SIMILARITY).  
FT VARIANT 499 499 A -> V.  
FT VARIANT 550 550 /FTIG-VAR\_004617.  
FT VARIANT 550 550 R -> Q.  
FT VARIANT 550 550 /FTIG-VAR\_004618.  
FT CONFLICT 404 404 M -> L (IN REF. 4).  
FT CONFLICT 517 517 F -> L (IN REF. 2 AND 4).  
FT CONFLICT 536 537 VA -> WH (IN REF. 2).  
SQ SEQUENCE 676 AA; 883EAL13797020D70 CRC64;  
  
Query Match 14.1%; Score 767; DB 1; Length 676;  
Best Local Similarity 32.4%; Pred. No. 1.1e-35;  
Matches 211; Conservative 113; Mismatches 264; Indels 64; Gaps 23;  
  
QY 444 FVYKAKSKIP-----LGGIPSPSTEOS-AKKYKKAENAHNPPLVLYGSMGTAEAGTAR 498  
DB 41 FLFRKKKEVEPFTKTIQTLSVRESSFVEKKKTKGRN-----IIVFGSQGTAEAFAN 95  
QY 499 DIADIAMSGFAPQVATLDH-----AGNLPREGAVLIV--TASY-NGHPDPAKQFVDWL 551  
DB 96 RLKSDAHRYGMRGMSADPEYDLADLSSLPEDNALVVFMTATYBGDPDQNAQDFYDWL 155  
QY 552 DQASADEVGVYRVSFGCCDKWATYQKVPV---PIDETLAAGAENIADGEADASD 608  
DB 156 QETDVD-LSGVFVAFVGLGNK---TYEHFNAMGYVDRKRLBOLGAQRIFELGLGDGDN 210  
QY 609 FEQTEWEHMHWSVAAVFNLDIENSEDNKSTLSQF---VDSA-----ADMPLAKMH-- 659  
DB 211 LEEDEFITREQFWPACVEHGEVTEATGEESIRQYELVVDHDAKQVYMGGRUKSYEN 270  
QY 660 -----GAFSTNVVASKELQPGSARSTRHLETEL-PKEASYQEGDHLGVIPRYEGI 710  
DB 271 QRPFPDAKNPFLAAVTTNRKLQ-GTERHLMHLELDISDSKIRYESGDHVAVYPANDSAL 329  
QY 711 VNRVTARFG--LDASQIRLEAEKEKLAHLPLAKTVSVEELQYVELODPVTRTOLRAMA 768  
DB 330 VNLQKILGADLDVMSLNLDSESNKKHPFPCPTSYRTALTYLDITNP-PRTNVLYEL 388  
QY 769 AKTVCPHPKVELEALE-----KQAYKEQVLAKRUTMLELLEKYPACEMKSEFTALPL 822  
DB 389 AQVASEPSQELLRLKMASSGEGKELYLSWVYARRHILAILQDCPSLRPPIDHLCLELP 448  
QY 823 SIRPRYISISSPRVDEKQASITVSVSGEANSYGEYKGIASNYL-AELQEGDT----- 876  
DB 449 RLQARYISASSKVNHPNSVHICAVVYETETAGRIN-KGVATNMLRAKEPAGENGGRAL 507  
QY 877 ITCFISTPOSEFTLPKDPETPLIMVPGTGVAPFGFVQARKOLKEQOSLGEAHLFYFC 936  
DB 508 VPMFVR--KSQELFPKATPVIMVPGTGVAPFGFVQARKOLKEQOSLGEAHLFYFC 565  
QY 937 RSPHEDLYOELENAQSEGIIT-LHTAFSRMPNPKTYVQHVMEQDGKLLIELLDQGAH 995  
DB 566 RRSDELYRELEAQLPHRDGALTNLVAFPSREQSH-KVYVQHLLAQDRHKLKLEGGAH 624  
QY 996 FYICGDSQMAVAEATLMKSYADHVQVSEADARLWLQLEEKGRYAKDWA 1047

Db 625 IIVCGDARNMARDVQNTFFDIIVAEIGAMEHAQAVDYIKKMTKGRYSLDWS 676  
RESULT 9  
NCPR\_CAVPO  
ID NCPR\_CAVPO STANDARD; PRT; 677 AA.  
AC P37039;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).  
GN POR.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Hartley;  
RX MEDLINE=93041995; PubMed=1420354;  
RA Ohguya S., Goda T., Ishizaki K., Kamataki T., Shinriki N.;  
RT "Molecular cloning and sequence analysis of guinea-pig NADPH-  
cytochrome P-450 oxidoreductase.";  
RL Biochim. Biophys. Acta 1171:103-105(1992).  
RN [2]  
RP ERRATUM.  
RX MEDLINE=93385164; PubMed=8373812;  
RA Ohguya S., Goda T., Ishizaki K., Kamataki T., Shinriki N.;  
RL Biochim. Biophys. Acta 1174:313-313(1993).  
CC -!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
CC -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2  
ferricytochrome.  
CC -!- COFACTOR: FAD AND FMN.  
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
CC -!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
REDUCTASE.  
CC -!- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO ORIGINATE FROM MOUSE.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL: D10498; BAA01385.1; -.  
DR PIR: S27158; S27158.  
DR HSP: P00388; IAMO.  
DR InterPro: IPR003097; FAD\_binding.  
DR InterPro: IPR001709; FPN\_cyt\_redtse.  
DR InterPro: IPR001094; Flavodoxin\_like.  
DR InterPro: IPR001226; Flavodoxin.  
DR InterPro: IPR001433; Oxred\_FAD/NAD(P).  
DR Pfam: PF00175; NAD\_binding; 1.  
DR Pfam: PF00258; flavodoxin; 1.  
DR Pfam: PF00667; FAD\_binding; 1.  
DR PRINTS: PR00369; FLAVODOXIN.  
DR PRINTS: PR00371; FPNCR.  
KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
KW Membrane; Acetylation.  
FT INIT\_MET 0  
FT MOD\_RES 1  
FT NP\_BIND 169 200 FWN (PYRIMIDINE PART) (BY SIMILARITY).  
FT NP\_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).  
FT NP\_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).  
FT NP\_BIND 528 546 NADP (RIBOSE PART) (BY SIMILARITY).  
FT NP\_BIND 622 638 NADP (ADP PART) (BY SIMILARITY).  
FT VARIANT 499 499 A -> V.  
FT VARIANT 550 550 /FTIG-VAR\_004617.  
FT VARIANT 550 550 R -> Q.  
FT VARIANT 550 550 /FTIG-VAR\_004618.  
FT CONFLICT 404 404 M -> L (IN REF. 4).  
FT CONFLICT 517 517 F -> L (IN REF. 2 AND 4).  
FT CONFLICT 536 537 VA -> WH (IN REF. 2).  
SQ SEQUENCE 676 AA; 883EAL13797020D70 CRC64;



Db 385 ELAEY--CSDEKDEFLRNMASTIT---PE-----GREKYQWIONSSRNIVHLEDI 431  
QY 808 PACEMKFSEPIALLPSIRPRYYISISSPRVDEKQASTVSVSSEAWSGYGEVKGITASNY 867  
Db 432 KSCRPIIDHICELPLRQPRYYISISSKLYPTNVHITAVLVQYETPTGRVN-KGVATSY 490  
QY 868 LAELOE--GDT-ITCFISTPQSEFTLPKDPETPLIMVGPOTGVAPFRGFVQARKOLKEQG 924  
Db 491 MKEKNPVGVEKVPVFEIR--KSQFRLPTKSEIPIIMVGPCTGLAPFRGFIQERQFLRDGS 548  
QY 925 QSLGEAHLFGCRSPHEDYLYQBELENAQSEGIITHTAFSPNPNQPKYVQVHMQDQK 984  
Db 549 KVVGDITLYFGCRKDEDEIYREBELOYQNGFTLTAKFSR--DQOGEKIYVTHLBQDAD 607  
QY 985 KLELL--DQAGHYICGDSQMAVEATLMKSYADVHOVSADARLWLQOLKEKGRYAK 1043  
Db 608 LIKWVIGEGKHGYICGDAKNMAYDVNLYLKILSTKGNMNSDVAQYIKKMEAKRYSA 667  
QY 1044 DWNA 1047  
Db 668 DVNS 671

## RESULT 11

NCPR\_DROME STANDARD; PRT; 679 AA.  
AC Q27597; Q9VMF2;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).  
GN CPR OR C011567.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7221;  
RN [1]  
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
RC STRAIN=Canton-S; TISSUE=Antenna;  
RX MEDLINE=97311413; PubMed=9168130;  
RA Hovenann B.T., Sehlmeier F., Malz J.;  
RT "Drosophila melanogaster NADPH-cytochrome P450 oxidoreductase:  
RT pronounced expression in antennae may be related to odorant  
RL Gene 189:213-219(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.D.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., M.G.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese H.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling R.C., Stapleton M., Strong R., Sun E.,  
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA "Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
CC -!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5. MAY FUNCTION TO  
CC CLEAR THE OLFACTORY ORGAN (ANTENNAE) FROM ACCUMULATING CHEMICALS.  
CC -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
CC ferriocytocrome.  
CC -!- COFACTOR: FAD AND FMN.  
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION (BY SIMILARITY).  
CC -!- TISSUE SPECIFICITY: HIGH IN ANTENNAE.  
CC -!- DEVELOPMENTAL STAGE: EMBRYOS AND ADULTS.  
CC -!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
CC NADPH+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
CC REDUCTASE.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: X91090; CAA63639.1; -  
CC EMBL: AF003613; AAF52367.1; -  
CC HSP: P16435; LBIC.  
CC Flybase: FBgn0015623; Cpr.  
CC InterPro: IPR003097; FAD\_binding.  
CC InterPro: IPR001709; FPN\_cyt\_redctse.  
CC InterPro: IPR001094; Flavodoxin\_like.  
CC InterPro: IPR001226; Flavodoxin.  
CC InterPro: IPR001433; Oxred\_FAD/NAD(P).  
CC Pfam: PF00175; NAD\_binding; 1.  
CC Pfam: PF00258; flavodoxin; 1.  
CC Pfam: PF00667; FAD\_binding; 1.  
CC PRINTS: PR00369; FLAVODOXIN.  
CC PRINTS: PR00371; FPNCR.  
CC Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
CC Membrane.  
KW NP\_BIND 176 207 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
FT NP\_BIND 320 331 FAD (ADP PART) (BY SIMILARITY).  
FT NP\_BIND 457 467 FAD (FLAVIN PART) (BY SIMILARITY).  
FT NP\_BIND 537 555 NADP (RIBOSE PART) (BY SIMILARITY).  
FT NP\_BIND 632 648 NADP (ADP PART) (BY SIMILARITY).  
FT CONFLICT 38 39 AA -> VT (IN REF. 1).  
FT CONFLICT 45 45 S -> T (IN REF. 1).  
FT CONFLICT 132 132 I -> T (IN REF. 1).  
SQ SEQUENCE 679 AA; 76346 MW; C6387C11A0EDB4A CRC64;

Query Match 13.3%; Score 725.5; DB 1; Length 679;  
Best Local Similarity 29.8%; Pred. No. 2.4e-33;  
Matches 191; Conservative 113; Mismatches 257; Indels 79; Gaps 21;  
QY 460 SPSTEQSAKKYKKKAENAHNTPLLVLYGSMCTAGSTARDLADIAWS---KGFA--POVA 514  
Db 67 SASDNSFIKKL-----ASGRSLVVFYGSQTGTGEFAGRLAKEGIRYLRKGVADPEEC 121

515 TLDS--HAGNLPREGAVLIIVTASNGHPPDNKAKQFVMDLQASADEKGVYRYSVFGCGDK 572  
122 DMEELLQKIDNSLAVFCLATYEGDPTNAMEFYEMITSGVDV-LSGLNAYVFLGNK 180  
573 NWATTYQKVPFIDETLAAGAENIADRGADSDDEGFEYEEWREHMSDVAAYFNLDI 632  
181 TY-EHYNKVAIYVDKREELGALNRFVGLGLGDDDDANIEDFITWKDRFWPACVDFHG--I 237  
633 ENSDNKSTLSQFVDSAADP-----LAKMH-----GAFSTNVVASKELQ 673  
238 EGGEEVLLIROYLLEQDPVDPDRIYTGELARLSHISQNPFPDPAKPFILAPKVNRELH 297  
674 QPSGARSTRHLEIPL-KEASYQEGDHLGVIPRNYEGIVNRVTRARFGLDAS--QQIRLE 729  
298 K-GGGRSCMHIELSIEGSKMYRDAYGDMVFPVNDKSLVEKLGQLCNADLDTVPSLINTD 356  
730 ABEKLAHL-----LAKTVSVEELLQYVELQDPVTRTQLRMAAKTV 772  
357 TDSKKHFPFPTTYRTALTHTYLEITAPRTHILKLAAY--CTDEKEKELLRSMA--SI 412  
773 CPPHKVEALLEKQAYKEOVLAKRLTLMLELKYAPACMKFSEFIALLPSIRPRYSIS 832  
413 SPE-----GREKQSWIQDACRNIVHILEDIKSCRPPIHVCELLPRLQPRYSIS 463  
833 SSPRVDEKQASITVSVSGEAWSGYGYKGIASNYLAELQ-----EGDTITCFISTPQSEF 888  
464 SSAKLHPTDHTVAVLVEYKTPGTGRIN-KGVATTYLNKQPOGSEEVKVPVFI--KSQF 520  
889 TLPKDPETPLMWPGTGVAPFRGVQARKQKQSGSLGEAHLYFCGRSPHEDYLOEE 948  
521 RLPTPETPIIMWPGTGLAPFRGFIQERFLRDEGTVGESILYFCGRKRSEDIYIESE 580  
949 LENAQSGEITHTAFSRMNPQKTYVOHVMEQDGKLIELLDQ--AHFYICGDSQMAP 1007  
581 LEWVKGTNLNKAASRDOCK-KVYVQHLLQDADLIWNVIGENKGFHYICGDAKNVAV 639  
1008 AVEATLMKSYADVHVSEADARLWQLEEKGRYAKDWA 1047  
640 DVNRILKILSTKGMSEADAVQYIKKMEAKRYSADVWS 679

RESULT 12  
NCPR\_SALT  
ID NCPR\_SALT STANDARD; PRT; 601 AA.  
AC P19618;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R)  
DE (Fragments).  
OS Salmo trutta (Brown trout).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protactinopterygii; Salmoniformes; Salmonidae; Salmo.  
OX NCBI\_Taxid=8032;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=880808061; PubMed=3116019;  
RA Urenjak J., Linder D., Lumper L.;  
RT "Structural comparison between the trout and mammalian hydrophilic  
domain of NADPH-cytochrome P-450 reductase.";  
RL J. Chromatogr. A 397:123-136(1987).  
CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
TO CYTOCHROME P450 IN MICROSOSES. IT CAN ALSO PROVIDE ELECTRON  
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
ferricytochrome.  
CC -1- COFACTOR: FAD AND FMN.  
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN

CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
REDUCTASE.  
CC PIR: A28577; A28577.  
DR HSP; P16435; IBLIC.  
DR InterPro; IPR001709; FPN\_cyt\_redctse.  
DR InterPro; IPR001094; Flavodoxin\_like.  
DR PRINTS; PR00369; Flavodoxin.  
DR PRINTS; PR00371; FPNCR.  
KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
KW Membrane.  
FT NON\_TER 1 1  
FT NON\_CONS 426 427  
FT NON\_CONS 434 435  
SQ SEQUENCE 601 AA; 68304 MW; BC801767DELD44C9 CRC64;  
Query Match 13.28; Score 723; DB 1; Length 601;  
Best Local Similarity 30.2%; Pred. No. 2.8e-33;  
Matches 195; Conservative 106; Mismatches 239; Indels 106; Gaps 21;  
Qy 459 PSPTEQSA--KKVRKKAENAHNTPLLVLYGSGNMGTAEGTARDLADIAMSKGFAPVATL 516  
Dy 5 PAPSTQETSFTEKMKTKGRN-----IVFYGSQGTGEEFANRLSKDAHRYGMSGMAADP 59  
Qy 517 D-----SHAGNLPREGAVLIIV--TASY-NGHPPDNKAKQFVMDLQASADEKGVYRYSVFGC 569  
Dy 60 EYDMSLSRLAEIGNSLAIFCMATYGECDPTDQNAQDFYDLW-QETDGLSGVNPVFPAL 118  
Qy 570 GDKNWTYQKVPFIDETLAAGAENIADRGADSDDEGFEYEEWREHMSDVAAYFN 629  
Dy 119 GDKTY-EHYNKVAIYVDKREELGALNRFVGLGLGDDDDANIEDFITWKDRFWPACVDFHG 177  
Qy 630 LDIENSNDKSTLSQFVDSAADPMAKMH-----GAFSTNVVASKELQ 669  
Dy 178 VEASGEDSSVROQYELK-----EHDNIMNKVYTGELGRKLSFETQKPPDKNPFAPVTVN 234  
Qy 670 KLOQPCASSTRHLEIPL-KEASYQEGDHLGVIPRNYEGIVNRVTRARFGLDASQIRL 728  
Dy 235 RKLKAGELHK-MHELVDTGSKTRYESGDHVAIVPTNTVIVNRGLQILGVLDLSDVSL 293  
Qy 729 EAEEEK-----LAHLPLAKTVSVBELQY-VELODPVTRTQLR 765  
Dy 294 NNLDESNKKHFPFPTTYRTALTHTYLDIHTPP--RTNVLYELAQYATDLKQENTDSMA 351  
Qy 766 AMAAKTVCPHPKVELEALLEKQAYKEOVLAKRLTLMLELKYAPACMKFSEFIALLPSIR 825  
Dy 352 SSAPE-----GKALYQSFVLENNRNILAILDPLSRPPIHVCELLPRLQ 397  
Qy 826 PRYSISSSPRVDEKQASITVSVSGEAWSGYGYKGIASNYLAELQEGDTITCFIST 883  
Dy 398 ARYSISASSSKVHPNSHICAVLV-----EYTKGVATTWLKVIYR----- 437  
Qy 884 PQSEFTLPKDPETPLMWPGTGVAPFRGVQARKQKQSGSLGEAHLYFCGRSPHEDY 943  
Dy 438 -KSQFRLPFRKASNPVIMVPGTGTAPMGFIQERGLWLGKESGVEGYVLYCGCRKHEEDY 496  
Qy 944 LYQEELENAQSGEITHTAFSRMNPQKTYVOHVMEQDGKLIELLDQAHFYICGD 1001  
Dy 497 LYQEELENAQSGEITHTAFSRMNPQKTYVOHVMEQDGKLIELLDQAHFYICGD 555  
Qy 1002 GSNAPAVEATLMKSYADVHVSEADARLWQLEEKGRYAKDWA 1047  
Dy 556 ARNARDVQTAFTAFYEAELGEGMTQTATDYIKKLMKTRYSQDWS 601

RESULT 13  
NCPR\_PHAU  
ID NCPR\_PHAU STANDARD; PRT; 690 AA.  
AC P37116;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).  
OS Phaseolus aureus (Mung bean) (Vigna radiata).



NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE REDUCTASE.

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EMBL; X69791; CAA49446.1; -;  
 EMBL; Y09417; CAA70571.1; -;  
 PIR; S31502; S31502.  
 HSSP; P00388; 1AMO.  
 InterPro; IPR003097; FAD\_Binding.  
 InterPro; IPR001709; FPN\_cyt\_redtse.  
 InterPro; IPR001094; Flavodoxin-like.  
 InterPro; IPR001226; Flavodoxin.  
 InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 Pfam; PF00175; NAD\_Binding; 1.  
 Pfam; PF00258; flavodoxin; 1.  
 Pfam; PF00667; FAD\_Binding; 1.  
 PRINTS; PR00369; FLAVODOXIN.  
 PRINTS; PR00371; FPNCR.  
 Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum; Membrane.

FT NP\_BIND 200 231 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 348 359 FAD (ADP PART) (BY SIMILARITY).  
 FT NP\_BIND 489 499 FAD (FLAVIN PART) (BY SIMILARITY).  
 FT NP\_BIND 567 585 NADP (RIBOSE PART) (BY SIMILARITY).  
 FT NP\_BIND 661 677 NADP (ADP PART) (BY SIMILARITY).  
 SQ SEQUENCE 714 AA; 78958 MW; DBDD9AF41374CF91 CRC64;

Query Match 12.98; Score 702; DB 1; Length 714;  
 Best Local Similarity 28.88; Pred. No. 5.4e-32;  
 Matches 189; Conservative 118; Mismatches 274; Indels 76; Gaps 18;

QY 445 VVAKSKKIPGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSGNMGTAGTARDLADIA 504  
 Db 79 VVEPKLIVPKSVVEPEIDEGKKK-----FTIFFGQTGTAEFGAKALAEAE 126  
 QY 505 MSK--GFAQVATLDSHAGN-----LPRGAVLIVTASY-NGHPPDNAAKQFVMDLQDA 554  
 Db 127 KARYEKAVIKVIDIDDAADDEEYERKETTALFFILATYGDGEPTDNRARFYKWFVEG 186  
 QY 555 S--ADEVKGVRYVFGCGKNAWTKYKVPFADITETLAAGAENIADRGADASDDFEGT 612  
 Db 187 NDRGDWLNQYGVFGLGNQY-EHFNKIADVDEKVAEQGKKRIVPLVLGDDDDQCIEDD 245  
 QY 613 YEEWREHWSVAAFYNFLDIENSEDNKSTLSLQFV-----DSAADMPLAKMHGAF 662  
 Db 246 FAARWENWPE-----LDNLLRDEDTTSTVTTAAIPEYRVVFPDKSDSLSEANGHA 299  
 QY 663 S-----TNVASKELQOPGASRTRHLELPEKA-SYQBGDHLGVIPR 705  
 Db 300 NGYANGNTVYDAQHPCRSNVAVRKELHTPASDRSCTHLDFDIAGTGLSYGTGDHGVYCD 359  
 QY 706 NYEGVNRVTRARFGDASQQIRLEAEKEKLAHL-----PLAKTVSVEELQVVELQDP 758  
 Db 360 NLSETVEAEELLNLPETVFSLHADKEDGTPLAGSSLPFPFPCTRTALTRALDNT 419  
 QY 759 VTRTOLRAMAKTVCPPHKVELEALLE---KQAYKEQVLAKRFLMELLEKYPACEMKFS 815  
 Db 420 PKKSALLAALAAADPNADRLKYLASPAQKDEYAQSILVANQSRSLLEVMFAEFPKAPLG 479  
 QY 816 EFI-ALLPSIPRPRYSISSPRVDEKQASTVSVSGEANSWGYGEYGIASNYLAE---L 871  
 Db 480 VFFAAIAPRLOPRYSISSSPRMAPSRHVTALVY-EKTPGGRIHKGVCSTWKNAPIL 538  
 QY 872 QEG-DTITCTFTSQSEFTLPKDPETPLIMVGPCTGVAPFRGVQARKQLKEQCSQAGEA 930  
 Db 539 EESRDCSWAPFVQSNFKLPADPKVPMIGPCTGLAPFRGLQERLALKEGAEELGTA 598

QY 931 HLXFGCRSPHEDLYOEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIEL 989  
 Db 599 VFFGCRNRKMDYIYEDLNHFLEIGALSELLVAFSR-EGTKQTVQHKMAEKASDIWRM 657  
 QY 990 LDQGAHFYICGDSQMAPAVEATLMKSVADYVQVSEADARLWLQQLQLEEKGYAKDVW 1046  
 Db 658 ISDGAYVYVCGDAKGMARDVHRTLHTIAEQSGSDSTQAEQVFNLQMTGRYLDRDV 714

RESULT 15  
 NOS2\_RAT STANDARD; PRT; 1147 AA.  
 AC Q06518; P97774; Q35765; Q35766; Q64558; Q64005; Q63267;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)  
 DE (Inducible NOS) (iNOS).  
 GN NOS2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Vascular smooth muscle.  
 RX MEDLINE=93191721; PubMed=7680561;  
 RA Nunokawa Y., Ishida N., Tanaka S.;  
 RT "Cloning of inducible nitric oxide synthase in rat vascular smooth  
 muscle cells.";  
 RL Biochem. Biophys. Res. Commun. 191:89-94(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar; TISSUE-Pancreatic islets;  
 RX MEDLINE=9530954; PubMed=7540573;  
 RA Karlson A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J.,  
 Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,  
 Mandrup-Poulsen T., Boel E., Nerup J.;  
 RT "Cloning and expression of cytokine-inducible nitric oxide synthase  
 cDNA from rat islets of Langerhans.";  
 RL Diabetes 44:753-758(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Astrocyes;  
 RX MEDLINE=94231594; PubMed=7513765;  
 RA Galea E., Reis D.J., Feinstein D.L.;  
 RT "Cloning and expression of inducible nitric oxide synthase from rat  
 astrocytes.";  
 RL J. Neurosci. Res. 37:406-414(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver.  
 RX MEDLINE=94039059; PubMed=7693462;  
 RA Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K.,  
 Kawasaki H., Sugimura T., Esumi H.;  
 RT "Molecular cloning of a cDNA encoding an inducible  
 calmodulin-dependent nitric-oxide synthase from rat liver and its  
 expression in COS 1 cells.";  
 RL Eur. J. Biochem. 217:37-43(1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE-Hepatocytes;  
 RX MEDLINE=93221515; PubMed=7682072;  
 RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;  
 RT "Hepatocytes and macrophages express an identical cytokine inducible  
 nitric oxide synthase gene.";  
 RL Biochem. Biophys. Res. Commun. 191:767-774(1993).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Aorta;  
 RX MEDLINE=94325351; PubMed=7519448;  
 RA Geng Y.J., Almquist M., Hansson G.K.;







Db 538 VLFATETGKSEALARDIAAL-FSYAFNTKVCMEQYKANTLEEQLLLVVTSTFGNGDCP 596  
Qy 542 DNAKOFVDWLDQASADVKGV---RYSVFGCGDKNWTYYOKVPAP---IDETLAAKGA 594  
Db 597 SNGOTL-----KSLFMKMKELGHTFRYAVFGLG-----SSMYPQCAFADHDOKLSHLGA 647  
Qy 595 ENTIADRGEDASDDFEGTYEWEHMHMSDVAAYFNLDIENS-----ED 637  
Db 648 SOLAPTGEDELSCQEDAFRSWAVQTFR--AACHTFDVRSKHICIIPKRYTSNATWEPEQ 705  
Qy 638 NKSTLSLQFVDSAADMLAKMH--GAPSTNVVASKELQOPGSRSTR--HLEIPLKEAS 693  
Db 706 YKLTQSPESLD--LNKALSSIHAKNVETMLKSLQNLQSEKSRITLLVQLTFFGSRGPs 763  
Qy 694 YQEGDHGIVIPRNYEGIVNRVTARFGLDAS---QOIRLEAEAE-----KLAHLPLAKTV 744  
Db 764 YLPGEHLGIFPGNQTALVQILERV-VDCSSPDQTVCLVLEDESGSYWVKDKRLP----PC 819  
Qy 745 SVEELLOY-VELQDPVTRTOLRAMAAKTVCPPHKVELEALLEKQAYKEQVLAKRLTMLEL 803  
Db 820 SLRQALTYFLDITTPPTQLQHLKAREATEETHRQLEALCQPSEYNDWKFSNNPTLEV 879  
Qy 804 LEKYPACEMKFSEFIALLPSIRPRYYSISSPRVDEKQASITYSVVSGEAWSGYGE-YKG 862  
Db 880 LEEFPSLRVPAFLLSQLPIKPRYYSISSQDHTPSEVHLTVAVVTYTRDQCGPLHHG 939  
Qy 863 IASNYLAELQEGDITTCFISTPOSEFTLPKDPETPLIMVGPGTGVAPFGFVQAR-KOLK 921  
Db 940 VCSTWINNLKPEDVPVPCFVRS-VSGFOLPEDPSQPCILIGPGTGIAPFRSFWQORLHDSQ 998  
Qy 922 EQGOSLGEAHLFGCRSPHEDYLYQEELENAQSEGII-TLHTAFSRMPNQPKTYVQHVME 980  
Db 999 HRGLKGRMTLVFGCRHPEEDHLYQEDQEMVRKGVLFQVHTGYSRPLPGPKPVVQDILQ 1058  
Qy 981 QD-GKKLIELL--DOGAHFYICGDGQOMAPAVEATLMKSYADVHQVSEADARLWLOLEE 1037  
Db 1059 KELADEVFSVLHGEQG-HLYVCGD-VRMARDVATTLAKLVAAKLNLSSEQVEDYFFOLKS 1116  
Qy 1038 KGRYAKDVW 1046  
Db 1117 QKRYHEDIF 1125

Search completed: May 29, 2003, 08:29:01  
Job time : 30 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:25:36 ; Search time 99 Seconds  
(without alignments)  
2181.186 Million cell updates/sec

Title: US-10-031-146-2

Perfect score: 5457

Sequence: 1 TTKEPQPTFGELKNLPL.....RLWLOLEEKGRYAKDWWAG 1048

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1736.5	31.8	1066	3 Q9Y8G7	Q9Y8G7 fusarium ox
2	1462.5	26.8	1115	3 Q9HGE0	Q9HGE0 gibberella
3	961	17.6	527	16 Q9RD76	Q9RD76 streptomyce
4	773.5	14.2	667	11 Q60451	Q60451 cricetus
5	745	13.7	719	10 Q40916	Q40916 pseudotsuga
6	739.5	13.6	692	10 Q9SB48	Q9SB48 arabidopsis
7	737.5	13.5	681	10 Q48937	Q48937 petroselinu
8	734.5	13.5	703	10 Q8VX49	Q8VX49 triticum ae
9	717	13.1	712	10 Q9AU06	Q9AU06 populus bal
10	714.5	13.1	692	10 Q39035	Q39035 arabidopsis
11	711.5	13.0	683	10 Q24424	Q24424 papaver som
12	711.5	13.0	692	10 Q9AU08	Q9AU08 populus bal
13	711	13.0	692	10 Q43235	Q43235 vicia sativ
14	710	13.0	656	10 Q9FVW7	Q9FVW7 triticum ae
15	709	13.0	711	10 Q9SUM3	Q9SUM3 arabidopsis
16	706	12.9	705	10 Q24425	Q24425 eschscholzi

17	705.5	12.9	588	10 Q96561	Q96561 helianthus
18	705	12.9	699	10 Q48938	Q48938 petroselinu
19	702.5	12.9	712	10 Q39036	Q39036 arabidopsis
20	695.5	12.7	704	10 Q04434	Q04434 pisum sativ
21	694	12.7	321	2 Q9ZHK0	Q9ZHK0 rhodococcus
22	691	12.7	712	10 Q9AU07	Q9AU07 populus bal
23	690.5	12.7	687	5 Q9NKV3	Q9NKV3 bombyx mori
24	685.5	12.6	1147	11 Q9ROW4	Q9ROW4 rattus norv
25	684.5	12.5	662	5 Q09590	Q09590 caenorhabdi
26	681.5	12.5	1311	6 Q9BDH6	Q9BDH6 equus cabal
27	680	12.5	701	5 P91655	P91655 drosophila
28	680	12.5	736	3 Q9HDG2	Q9HDG2 phanerocha
29	669.5	12.3	1147	11 Q9QW28	Q9QW28 rattus sp.
30	668	12.2	690	3 Q9HG14	Q9HG14 phanerocha
31	667.5	12.2	671	3 Q9HFV3	Q9HFV3 thizopus st
32	665.5	12.2	1145	11 Q8RA10	Q8RA10 mus musculu
33	661	12.1	1114	4 Q9A994	Q9A994 homo sapien
34	658.5	12.1	1154	6 Q97604	Q97604 canis fami
35	657.5	12.0	693	3 Q00141	Q00141 aspergillus
36	651.5	11.9	759	3 Q9C498	Q9C498 rhodotorula
37	650.5	11.9	945	6 Q9N175	Q9N175 ovis aries
38	644.5	11.8	730	3 Q8X1W0	Q8X1W0 coriolus ve
39	636.5	11.7	607	16 Q9KE76	Q9KE76 bacillus ha
40	628.5	11.5	605	16 Q32214	Q32214 bacillus su
41	627.5	11.5	506	10 Q96560	Q96560 helianthus
42	617.5	11.3	710	3 Q9P4E2	Q9P4E2 cunningham
43	615.5	11.3	1055	5 Q968Y4	Q968Y4 physarum po
44	605.5	11.1	1206	11 Q9WTK6	Q9WTK6 cavia porce
45	597.5	10.9	1205	6 Q9TUX8	Q9TUX8 canis fami

#### ALIGNMENTS

#### RESULT 1

ID	Q9Y8G7	PRELIMINARY;	PRT;	1066 AA.
AC	Q9Y8G7;			
DT	01-NOV-1999	(TrEMBLrel. 12, Created)		
DT	01-NOV-1999	(TrEMBLrel. 12, Last sequence update)		
DT	01-MAR-2002	(TrEMBLrel. 20, Last annotation update)		
DE	Bifunctional P-450:NADPH-P450 reductase protein (Fatty acid omega-			
DE	hydroxylase) (P450foxy) [includes: cytochrome P450 505 (EC 1.14.14.1);			
DE	NADPH-cytochrome P450 reductase (EC 1.6.2.4)].			
GN	CYP505.			
OS	Fusarium oxysporum.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreales; mitosporic Hypocreales; Fusarium.			
OX	NCBI_TaxID=5507;			
RN	[1]			
RP	SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.			
RC	STRAIN-MT-811;			
RC	MEDLINE=20564350; PubMed=10995755;			
RA	Kitazume T., Takaya N., Nakayama N., Shoun H.;			
RT	"Fusarium oxysporum fatty-acid subterminal hydroxylase (CYP505) is a			
RT	membrane-bound eukaryotic counterpart of Bacillus megaterium			
RT	cytochrome P450BM3."			
RL	J. Biol. Chem. 275:39734-39740(2000).			
RN	[2]			
RP	FUNCTION, AND SUBCELLULAR LOCATION.			
RC	STRAIN-MT-811;			
RC	MEDLINE=96271003; PubMed=8830036;			
RA	Nakayama N., Takemae A., Shoun H.;			
RT	"Cytochrome P450foxy, a catalytically self-sufficient fatty acid			
RT	hydroxylase of the fungus Fusarium oxysporum."			
RL	J. Biochem. 119:435-440(1996).			
CC	-1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. SHOWS HIGHEST			
CC	ACTIVITY TOWARD FATTY ACIDS WITH A CHAIN LENGTH OF 12-14 CARBONS.			
CC	THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP			
CC	TO CYTOCHROME P450.			
CC	-1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +			
CC	OXIDIZED FLAVOPROTEIN + H(2O).			
CC	-1- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) + 2			

Db.	605	DSTLEKRGTRGLVPMGSADAATSDMFSDFAWEDIVLWPGLKKEKYKISDESQGGKGLL-	663
Qy	644	LQFVDSAADPLAKMHGAFSTNNVASKELQPGSARSTRHLELFLPKASVQGDHLGVI	703
Db	664	---VEVSTPKTSLRQDVEALVVAEKTLLTKSGPAK--KHIEQLPSAMTYKAGDYLAAIL	718
Qy	704	PRNVEGTNRVTRARFGLDASQOIRLEAAEELKLAHLPLAKTVSVSEELIQ-XVELOQDPVTR	762
Db	719	PLNPKSTVARVERFSLAWDSFLKIQSEGP--ITLPTNVAISAFDVSAIVLSQSPATKR	776
Qy	763	QLRMAAKTVCPPHKVELEALLKEQAYKEQVLAKRTMLLELKKYPACEMKMFSEFIALLP	822
Db	777	NILALAEATEDKDTIQELER-LAGDAYQAYEISPKRVSVLQLEKFFPAVALPISSYLAMLP	835
Qy	823	SIRPRYYSISSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFIS	882
Db	836	PMVRQYISISSFPADSPKUTLLSYLDAPSLGQGHVGVATNUSHLTAGDKLHVSVR	895
Qy	883	TPOSEFTLPKDPE-TPLIMVPGTGVAPFRGFVQARKQKEQOQSLEAHLYFCGRSPHE	941
Db	896	ASSEAFHLPDAEKTPIICVAAUGTLAPLGRGFTQERRAAMLAGEITLAPALLFTGCRNPEI	955
Qy	942	DYLYQEELENAQSEGIITLHTASRMPNQK--TYVOHVMQDGKKLIELLDGGAHFYIC	999
Db	956	DDLVAEEFERWEKMGAVDVRRAYSRATDKSEGCKYVQDRYVHYHBRADVFKVMDQGA	1015
Qy	1000	GDGSQMAPAVE----ATLMKSYADVHVSEADARLWLOOLEKGRYAKDVW	1046
Db	1016	G-SREIGKAVEDVCVRLAIEKAQONGRDVTEEMARAWFERSRNE-RFATDVF	1065

RESULT 2

Q9HGEO PRELIMINARY; PRT; 1115 AA.

ID QHGE0

AC QHGE0;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Fun6p.

DE Fun6.

OS *Gibberella moniliformis*.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocreales; Nectriaceae; Gibberella.

ON NCBI\_TaxID=117187;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=M-3125;

RA Proctor R.H., Seo J.-A., Plattner R.D.;

RT "Characterization of four clustered and coregulated genes associated with fumonisin biosynthesis in *Fusarium verticillioides*.";

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

CC EMBL: AF155773; AAG27132.1; -.

DR HSP; P00388; IJ92.

DR InterPro; IPR001128; Cytochrome\_P450.

DR InterPro; IPR003097; FAD\_binding.

DR InterPro; IPR001094; Flavodoxin\_like.

DR InterPro; IPR001226; Flavodoxin.

DR InterPro; IPR001709; FPN\_cyt\_redctse.

DR InterPro; IPR001433; Oxred\_FAD/NAD(P).

DR Pfam; PF00667; FAD\_binding; 1.

DR Pfam; PF00258; flavodoxin; 1.

DR Pfam; PF00175; NAD\_binding; 1.

DR Pfam; PF00067; p450; 1.

DR PRINTS; PR00369; FLAVODOXIN.

DR PRINTS; PR00371; FPNCR.

DR PRINTS; PR00385; P450.

DR PROSITE; PS00086; CYTOCHROME\_P450; UNKNOWN\_1.

KW Heme; Monooxygenase; Oxidoreductase.

SQ SEQUENCE 1115 AA; 123276 MW; 5C6D2B947AE86C25 CRC64;

Query Match 26.8%; Score 1462.5; DB 3; Length 1115;



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Qy 56 RUIKACDESRFDKNLSQALKEFVDFADGDLFTSWTHEKNWKAHNLIPFSQQAMGY 115
Db 82 ALAADLAEARFAKHVGLGANLFPVAGDLGTAYNHEPNWQLAHDVLPAGFSREAMAGY 141
Qy 116 HAMVYDIAVOLVQKWERLNAD- EHIEVPEDMTRLTDTIGLCGFNYRFSFYDQHPPI 174
Db 142 HYMLDVAARLTGHWDLAEASGRAVDPGDMTKLITLETIARTGFGHDFGSFERSLUHPV 201
Qy 175 TSKWRALDEAMNKLQAN- ---PDDP- AYDENKRQOEDIKVMNDLVDRKIIADRAK- --- 225
Db 202 TAMVGTGLGY- ---QRLNTVPAPLAPMLLRDASRNAADIHLNRTVDDLVRERRANGST 257
Qy 226 ----SGBQSDDLTHMLNGKDPETGEPLDENIRQIITFLTAGHETTSGLLSFALYPL 280
Db 258 GGGTSGSGSGLDLRMDLETNHTRTGERLSQPNVRQVITFLVAGHETTSGLLSFALHYL 317
Qy 281 VKNPHVLQKAAFEARVLVD- PVPSYKQVKQLKTVGMVLNEALRLWPTAPAFSLYAKEDT 339
Db 318 AQHPDVAARAEADVWVGDTAPGYEQVAKLRYVRVLDESRLWPTAPGFAREAREDT 377
Qy 340 VLGGYPLEKGDELWVLIPLQHROKTITWGDVVEFPERFENESATPQ- --HAFKPFNGCQ 397
Db 378 VLGGTHPMRRGAWALVITGMUHRDPEVWGDAERFDPDFDAKAVRSRAPHFTKPFCTGA 437
Qy 398 RACIGQCFALHEATVLGMLMKHDFDEHDHNYELDIKETLTLKPEGVYVKAASKKIPLGG 457
Db 438 RACIGQFALHEATVLGLLLRVELAPEPGYRLRYTERLTLMPEGRLHLVYR- ---TNA 494
Qy 458 IPSPSTEQSAKKVRKKAENANTP 481
Db 495 APAPGRRTAAPGAADADGDTVSAP 518

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RESULT 4	Q60451	PRELIMINARY;	PRT;	667 AA.
ID	Q60451;			
AC	Q60451;			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)		
DE	NADPH-cytochrome P450 oxidoreductase.			
OS	Cricetulus griseus (Chinese hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Cricetulus.			
ON	NCBI_TaxID=10029;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-GOLDEN;			
RA	Ohguya S., Goda T., Hoshino T., Shinriki N., Kamataki T.;			
RT	"High-red yeast, construction of a novel strain of <i>Saccharomyces cerevisiae</i> stably exerting high activity of hamster cytochrome P450 reductase";			
RT	RT			
RL	Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; D83230; BAAL1856.1; ;			
DR	HSP; P00388; IAMO;			
DR	InterPro; IPR003097; FAD_binding.			
DR	InterPro; IPR001094; Flavodoxin-like.			
DR	InterPro; IPR001226; Flavodoxin.			
DR	InterPro; IPR001709; FPN_cyt_redctse.			
DR	InterPro; IPR001433; Oxred_FAD/NAD(P).			
DR	Pfam; PF00667; FAD_binding; 1.			
DR	Pfam; PF00258; flavodoxin; 1.			
DR	Pfam; PF00175; NAD_binding; 1.			
DR	PRINTS; PR00369; FLAVODOXIN.			
DR	PRINTS; PR00371; FPNCR.			
KW	NADP.			
SEQUENCE	667 AA; 75850 MW; 2023PF43DF4C1EF07			CRG64;

Qy	444	FVAKSKKIPLGG---IPSPSTEQA---KKVRKKAENAHTPTLVLVYCSNMGTAEGTAR	499
Dd		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Dd	31	FIFRKKKEEVPEFSKIQATPSVKRESSFVKMKKTGRN-----IIVFYGSQTGAEPAN	85
Qy	499	LIADIMSKGFAPQATLDSH-----AGNLPR--EGAVLIVTASY-NGHPDPNAKQFVDWL	551
Dd		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Dd	86	RLSDAHRYGMRGSADPEEYDLADLSLPEIDTKSLVFCMATYGEQDPTDNAODFYDWL	145
Qy	552	DOASADEVKGVYSVFEGCGDNWATTYQKVA-----FIDETLAAGAENIADRGEADASD	608
Dd		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Dd	146	QETDWD-LTGKVFAVFLGNK-----TYEHFNMGKYVDQRLEQLAQRIELGLGDGDN	200
Qy	609	PEGTYEWREHMSDVAAIFYNLDIENSNDKSTLSL---QFVDSA-----ADMPLAKMH--	659
Dd		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Dd	201	LEEDFITWREQFWPAVCFFGVEATGESSIRQYELLVHEDIIDAAKVVTGMGRLLKSYEN	260
Qy	660	-----GAFSTNVASKELQQPCRSABSTRHLEIEL-PKEASYQEQHGLGVIPNYEGI	710
Dd		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Dd	261	KQPFDKPNPFLAAYTTNRKLNQ-GTERHLMLHELDISDKIRYESGDHVAVYPANDSTL	319
Qy	711	VNRYTARFGLDASQOI---RLEAEEBKLAHLPLAKTVSVEELLOVELQDPVRTQLRAM	767
Dd		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Dd	320	VNOIGEILGADDVMSLNLDSESNKKHPPCPTYRT-ALTYILDITNP-PRTNLYYE	377
Qy	768	AAKTVCCP-----HKVEALELKQAYKEOVLAKRLFMLELEKYPACEMKFSEFIALL	821
Dd		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Dd	378	LAQYASEPSEQQLHKKNASSGEGKELYLSWVEARRHILATLDQYPSLRPPIDHLCCELL	437
Qy	822	PSIRPYRYSISSRPVDEKOASTIVSVVSGEANSYGEYKGTSNYL-AELOEGDT----	876
Dd		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Dd	438	PLQARYYSIASSSKVPNSVHICAVAVEYEAKSGRVN-KGVATSWLRAKEPAGEGRRRA	496
Qy	877	-ITCFISTPQSEFTLPKDPTPLIMVGPGTGVPAPRGFEVQARKOLKEQGQSILGEAHLYFG	935
Dd		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Dd	497	LVPMEVR--KSQRLPKSVTPVIMVGPGTGIAPEPMGFIOERAWLREGQKEVGETLLYYG	554
Qy	936	CRSPHEDYLQBELENQAQSEGIIT-LHTAFSRMPNQPKTYVQHYVMQDGKLIIELDQ-G	993
Dd		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Dd	555	CRRSDEDYLYREELAREFHDKGALTQLNVAFSR-EQAHKVYVVOHLLKRDRHLWKLIHEGG	613
Qy	994	AHFYCIGDGSOMAPAVEATLMKSVADVHOVSEADARLWLOOLEEKGRYAKDVWA	1047
Dd		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
Dd	614	AHIYVCGDARNMAKDQNTFYDIIAEFGPMHAQVDDVKKLMTKGRSLDWS	667
RESULT	5		
ID	Q40916	PRELIMINARY;	PRT; 719 AA.
AC	Q40916;		
DT	01-NOV-1996	(TrEMBLrel. 01, Created)	
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)	
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)	
DE	NADPH-cytochrome P450 reductase (EC 1.6.2.4).		
GN	CPr1.		
OS	Pseudotsuga menziesii (Douglas-fir).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pseudotsuga.		
OX	NCBI_TaxID=3357;		
RN	[1]		
RN	SEQUENCE OF 1-44 FROM N.A.		
RC	STRAIN={MIRB} FRANCO; TISSUE=SEEDLING;		
RC	Tranbarger T.J., Misra S.;		
RT	"The molecular characterization of a set of cDNAs differentially		
RT	expressed during Douglas-fir germination and early seedling		
RT	development.";		
RL	Physiol. Plantarum 95:456-464(1995).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN={MIRB} FRANCO; TISSUE=SEEDLING;		
RC	Tranbarger T.;		
RN	submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.		
RN	[3]		



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Db 64 PKSLMAKDEDDLDLG-----SGKTRVSIFFGTGTGTAGFAKAL 103
QY 501 AD--IAMSKGFAPOVATFLDSHAGN-----LPREGAVLIVTASY-NGHPPDNNAKORVDW 550
Db 104 SEELKARYEAAVVDLDYADDDOYEKLEKELAFVCVATYVGDGETDNNARFYKW 163
QY 551 LQASADEVK--GVRSVFCGDKNWTATYQKVPAFIDETLAAGAENIADRGAEADSD 608
Db 164 FTEENERDIKLQALAYGVFALGNQY-EHENKIGIVLDEELCKGAKRLIEVGLGDDQS 222
QY 609 FEGTYEWRHMSDVAAFNLD- IENSEDKS-----TSLQ 645
Db 223 IEDDFNAWKESLWSE-----LDKLLKDEDDKSVATPYTAVIPEYRVVTHDPRFTQKSM 276
QY 646 FVDSADMLAKMHGAFSTNVVASKELQOPGSASTRHLIELPKEA-SYQEGDHLGVIP 704
Db 277 ESNVANGNTIDIHFCRCVDVAVQKELHESDRSCIHLEFDISRTGITTYETGDHVGVA 336
QY 705 RNYEGIVNRVTARFGLDASQIIRLEAEELKLAHLPLAKTVSV-----EELQYVEL 755
Db 337 ENHVEIVEEAGKLGHSLLDVFSLHADKEDGS--PLESAVPPPPPGPCTLTGLARYADL 394
QY 756 QDPVTRTOLRAMAAKTVCPHPKVELEALLE---KQAYKEQVLAKRLTLMLELKYIPACEM 812
Db 395 LNPFRKSALVALAAYATEPSEAEKHLTSPDGKDEYSQWIVASQRSLLLEVMAAFPSAKP 454
QY 813 KFSEFT-ALLPSIRPRYISISSPRVDEKQASITVSVSGEAMSGYGEYKGIASNYL--- 868
Db 455 PLGVFAAIAPLQPRYISISSPRLAPSRVHVSALVYGTPTTG-RHKGVCSWTWKNNA 513
QY 869 ---AELQEGTITCFSTPQSEFTLPKDPETPLIMVPGTGVAPFRGFVQARKQLEQOG 925
Db 514 VPAEKSHESGADIFIRA--SNEKLPSPSTPIVMVPGTGLAPFRGFQERMAKLEDGE 571
QY 926 SLGEAHLXGCRSPHEDYLYQOELENAQSEGIIT-LHTAFSRMPNPKTYVQHVMEQDGK 984
Db 572 ELGSSLLFFGCRNQMDFIYEDELNNFVDQGVISELIMAFSREGAO-KEYVQHKMEKAA 630
QY 985 KLIELDQGAHFYICGDSQMAPAVEATLMKSYADYVQVSEADARLWLOOLEKGRYAKD 1044
Db 631 QVWDLIKEGYLVCGDAKGMDRVHRTLHTIIVQEGEGVSSSEAEALVKLQTEGYLRD 690
QY 1045 VW 1046
Db 691 VW 692

RESULT 7
O48937 PRELIMINARY; PRT; 681 AA.
AC O48937;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADPH cytochrome P450 reductase (EC 1.6.2.4).
GN CPR2.
OS Petroselinum crispum (Parsley) (Petroselinum hortense).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
OX NCBI_Taxid=4043;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98070859; PubMed=9405720;
RA Koopmann E., Hahlbrock K.;
RT "Differentially regulated NADPH:cytochrome P450 oxidoreductases in
RT parsley.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:14954-14959(1997).
DR EMBL; AF024634; AAB97736.1; -
DR HSSP; P00388; IAM0.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.

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DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_reductase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Oxidoreductase.
SQ SEQUENCE 681 AA; 75674 MW; C67AD80E8BAE0F6 CRC64;

Query Match 13.5%; Score 737.5; DB 10; Length 681;
Best Local Similarity 30.7%; Pred. No. 7.4e-38;
Matches 200; Conservative 104; Mismatches 275; Indels 73; Gaps 18;

QY 449 KSKKIPILGGIPSPSTQSAKKVKKKAENAHNTPLLVLYGSMGTAGETARDLADIAMSGK 508
Db 49 KSEVPKLIYPKVKEIEDEVDGKKK-----VTVFQGTGTAGEGFAKAEAKARY 100
QY 509 FAP--QVATLDSHA-----GNLPREGAVLIVTASY-NGHPPDNNAKQFVDWLDQA--SA 556
Db 101 ERAKFRVVDLDYAADEDEYEAKFKESPAFFLATYGDGETDNNARFYKWFSEEEKG 160
QY 557 DEVKGVRSYVFCGDKNWTATYQKVPAFIDETLAAGAENIADRGAEADSDDFEGTYEEW 616
Db 161 DWLNLQYGVFGLGNQY-EHFNKIAKVVDDGLADQAKRIVEVGMGDDDDQCIEDDFTAW 219
QY 617 REHMSD-----VAAYFNLDIENSEDNKSTLSLQFVDSAA 651
Db 220 RELVWPELKLLEDDEDTSAATPYTAALVLEYRVVVDYDQDLDATFLDSLSTQNGHTVHDA- 278
QY 652 DMPLAKMHGAFSTNVVASKELQOPGSASTRHLIELPKEA-SYQEGDHLGVIPRYVEGI 710
Db 279 -----QHPCRS-SVAAKKELHKKPASDRSCIHLEFDISHTGLAYETGDHVGVCENLVEI 331
QY 711 VNRVTARFGLDASQITRLEAEKEKLAHL-----PLAKTVSVEELQVYVLEQDPVTRTQ 763
Db 332 VEEAEKLLGMQPNYTSVHIDDEDGTPLTGGSLPPPPPPCTVRSALAKYADLLSPKKA 391
QY 764 LRMAAAKTVCPHPKVELEALLE---KQAYKEQVLAKRLTLMLELKYIPACEMKFSFIA- 819
Db 392 LIALAAHSDPTEADRLRLASAPAGDEYAQWVASHRSLLEVLAEFFPAKPLGVFFAS 451
QY 820 LLPSIRPRYISISSPRVDEKQASITVSVSGEAMSGYGEYKGIASNYL---AELQEG-D 875
Db 452 VAPRLQPRYISISSPRVPSRIHVTALVYEKTPTG-RHKGVCSWTWKNNAVSLSESHD 510
QY 876 TITCFISTPQSEFTLPKDPETPLIMVPGTGVAPFRGFVQARKQLEKQSGSLGEAHLVFG 935
Db 511 CSWAPIFVRQSNFKLPSTKVPITIMIGTGLAPFRGFLQERQALDAGALGTAVLYFG 570
QY 936 CRSPHEDYLYQOELEN-AQSEGIITLHTAFSRMPNPKTYVQHVMEQDGKLLIELDQGA 994
Db 571 CNRNLDIFIYDELNKLFVSGSISELIVAFSR-EGTKYEVQHKMLQKASEIWNLLISEGA 629
QY 995 HFYICGDSQMAPAVEATLMKSYADYVQVSEADARLWLOOLEKGRYAKDW 1046
Db 630 YIYVCGDAKGMDRVHRLHTIAEQOGLDSSKSAESWKNLQMTGRLYLRDW 681

RESULT 8
O48937 PRELIMINARY; PRT; 703 AA.
ID O48937;
AC O48937;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cytochrome P450 reductase (EC 1.6.2.4).
GN R2.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.

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Db 601 GCNRKMDFIYEDLNFFVESGALSELVAFSR-EGPTKEYVQHKMKQKASDIWNISQ 659
QY 994 AHFYICGDSOMAPAVEATLMKSYADVHVSEADARLWLQOLEKRGYAKDVW 1046
Db 660 GYLYVCGDAKMAKDVHRLHTIVQEGSLDNSKTESFVKSLOMNGRYLDDW 712

RESULT 10
Q39035 PRELIMINARY; PRT; 692 AA.
AC Q39035;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADPH-ferrihemoprotein reductase.
GN ATR1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEYNH; TISSUE=SEEDLING;
RA Mignote-Vieux C., Kazmaier M., Lacroute F., Pompon D.M.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; X65016; CAA46814.1; -.
DR HSSP; P00388; IAMO.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_reductse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW NADP.
SQ SEQUENCE 692 AA; 76768 MW; 5E0216F008B5D49E CRC64;

Query Match 13.1%; Score 714.5; DB 10; Length 692;
Best Local Similarity 29.2%; Pred. No. 2.1e-36;
Matches 193; Conservative 119; Mismatches 261; Indels 89; Gaps 19;

QY 441 PEGVVVAKSKKIPLAGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSGNMGTAGTARDL 500
Db 64 PKSLMAKDEDDLDLG-----SGKTRVSIFFTGTGTGAEGFAKAL 103

QY 501 AD--IAMSGFAPQVATLDSHAGN-----LPREGAVLIVTASY-NGHPPDNNAKQFVDM 550
Db 104 SEBIKARYEKAQVVDLDYAADDDQYBEKLLKETLAFPCVATYGDGPTDNNARFSKW 163

QY 551 LQASADEVK--GVRYSVFGCGDKNATYQKVPATIDETLAAKGAENIADGEADSD 608
Db 164 FTEENERDLKQALATGVFALGNRQY-EHFNKIGIVLDEELCKKAKRLIEVLGLGDDOS 222

QY 609 FEITYEWEHWMSSDVAAYFNLD-IENSEDNKS-----TSLQ 645
Db 223 IEDDENAKESLWSE-----LQKLLKDEDDKSVATPYTAVIPEYRVVTHDPRFTQKSM 276

QY 646 FVDSAADMLAKMHGAFSTNVVASKELQOPGSGARSTRHLEIPLKEA-SYQEGDHLGVTP 704
Db 277 ESNVANGNTTIDIHPCRDVAVQKELHTHESDRSCIHFLEFIDISRTGITETGDHGVYA 336

QY 705 RNYEGVNVNRTARFGLDASQIRLEAEKLAHLPLAKTVSV-----EELLYVEL 755
Db 337 ENHVEIVEAGKLLGSLDLSVSIHADKEDGS--PLESAPPPPGPCFLTGLTGLIARYDL 394

QY 756 QDPVTRTQLRAAMAKTVCPHPHVELFALLE---KQAYKEQVLAKRLTLMLELLEKYPACEM 812
Db 395 LNPPRKSALVALAAYATEPSEAEKLLKHLTSPDKDEYSQWIVASQRSLEVMFAFPsAKP 454
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QY 813 KFSEFI-ALLPSIRPRYSISSPRVDEKQASITVSVSGEAWSGYGEYKGIASNYL--- 868
Db 455 PLGVFFAATAPRLQPRYSISSCQDWPASRVHVTYSALVYGPPTG-RIHKGVCSTWKNKA 513
QY 869 ---AEIQEGDITTCFISTEQSEFTLPKDPETPLIMVPGTGVAPPRGFTVOARKQLKEQO 925
Db 514 VPAEKSHCEGAPIFIRA--SNFKLPSPSTPIVMVPGTGLTAPPRGFTLQERNALKEDGE 571
QY 926 SLGEAHLFYGCRSPHEDYLOELENAQSEGIIT-LHTAFSRMPNPKTYVQHVMEQDGK 984
Db 572 ELGSSLLFFGCRNRQMDFIYEDLNFFVQGVLSIELIMAFSREGAQ-KEYVQHKMKKAA 630
QY 985 KLIELDQGAHFYICGDSQMAPAVEATLMKSYADVHVSEADARLWLQOLEKRGYAKD 1044
Db 631 QVWDLIKEGYLYVCGDAKGMARDVHRTLHTIVQEGVSSSEAEAIKVKIQTGEGRYLDR 690
QY 1045 VW 1046
Db 691 VW 692

RESULT 11
O24424 PRELIMINARY; PRT; 683 AA.
AC O24424;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADPH-ferrihemoprotein oxidoreductase (EC 1.6.2.4).
OS Papaver somniferum (Opium poppy).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Papaveraceae; Papaver.
OX NCBI_TaxID=3469;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98096363; PubMed=9434750;
RA Rosco A., Pauli H.H., Priesner W., Kutchan T.M.;
RT "Cloning and heterologous expression of NADPH-cytochrome P450
RT reductases from the Papaveraceae.";
RL Arch. Biochem. Biophys. 348:369-377(1997).
DR EMBL; U67185; AAC05021.1; -.
DR HSSP; P00388; IAMO.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_reductse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Oxidoreductase.
SQ SEQUENCE 683 AA; 75888 MW; E07BD5E5EA8DE002 CRC64;

Query Match 13.0%; Score 711.5; DB 10; Length 683;
Best Local Similarity 30.3%; Pred. No. 3.2e-36;
Matches 191; Conservative 113; Mismatches 263; Indels 63; Gaps 20;

QY 470 VRKKAENAHNTP-----LLVLYGSGNMGTAGTARDLAD--IAMSGFAPQVATLDSHAG-- 521
Db 64 IDKEEEIEIVDPGKLTITFTGTGTGAEGFAKALAEIKAKYKKAIVKVVLDLDDYAAD 123
QY 522 -----NLPREGAVLIVTASY-NGHPPDNNAKQFVDMLDQ--ASADEVKGVRYSVFGCGDKN 573
Db 124 DQYEKLLKESLVFFWVATYGDGPTDNNARVYKWTQEHERGEWLOQLTYGVFGLGNQ 183
QY 574 WATTYQKVPATIDETLAAKGAENIADGEADSDDFEGTYEWEHWMSSD----- 623
Db 184 Y-EHFNKIAVDVDEQLGKQAKRIVQVGLGDDQDCTEDDFTAWRELLWTLELDQLLKDEDA 242
QY 624 -----VAAFNLDIENSEDNKSTLSLQFVDSA-ADMLAKMHGAFSTNVVASKELQO 674
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Db 243 APSVATPYIATVPEYRVVHETTTVAALDDKHINTANGDVAFDILHPC-RTIIVAQOQRELHK 301
QY 675 PGSARSTRHLEIELP-KEASYQSGDHLGVIPRNVGIVNRTARFG--LDASQOIRLEAE 731
Db 302 PKSDRSCIHLEFDISGSLTYEGDVGVAENCDTEVEAGKLLGQPLDLLFSIHTDKE 361
QY 732 EEKLAHLPLAKTVSV-----EELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEA 782
Db 362 DGS-----POGSSLPFPFGPCTLRSLARVADLLNPPRKASLTALSAHASPVEAERLRF 417
QY 783 L---LEKQAYKEOVLAKRLTMELEKYPACEMKFSEFI-ALLPSIRPRYISYSSSPRVD 838
Db 418 LSSPLGKNEYSKVVGSQSRLLSEMAEFPSAKPLGVFFAAVAPRPPRYISYSSSPKFA 477
QY 839 EKQASITVSVSGEAWSGYGEYKGIASNYLAELQEGDT-ITCFISTPQSEFTLPKOPETP 897
Db 478 PSRIHYTCALVYGOSTPG-NVHRGVCSTWKKHVPQDSWAPFVRT--SNFKLPADPSTP 534
QY 898 LIMVGPCTGVAPRFGVQARKOLKEQOQSLGEAHLYFGCRSPHEDYLYQBELENAOSEGI 957
Db 535 IIMVGPCTGLAPRFGFLQERMAKENGALGPALVFFGCRNRNMDFIYEDELNNFVRGV 594
QY 958 IT-LHTAFSRMPNPKTYVQHVMEQDGKLLIELLDQGAHYICGDSQMAPAVEATLMKS 1016
Db 595 ISELVAFSR-EGEKKEYVOHKWMEKATDVNNVISGDYLYVCGDAKGMAVDVHRTLHTI 653
QY 1017 YADVHVSEADARLWLQLEEKRYAKDVW 1046
Db 654 AQOGPMSESSAAEAANKLQVEERYLEDVW 683

RESULT 12
Q9AU08 PRELIMINARY; PRT; 692 AA.
ID Q9AU08 PRELIMINARY; PRT; 692 AA.
AC Q9AU08; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADPH-cytochrome P450 oxidoreductase isoform 1.
OS Populus balsamifera subsp. trichocarpa x Populus deltoides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Salicaceae; Populus.
OX NCBI_TaxID=3695;
RN [1]
RP SEQUENCE FROM N.A.
RA RO D.-K., Douglas C.;
RT "Functional characterization of cytochrome P450 reductase from the
RL hybrid poplar (Populus trichocarpa x P. deltoides).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF302496; AAK15259.1; -
DR HSSP; P00388; IAMO.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
SQ SEQUENCE 692 AA; 76725 MW; 7AA8CC78B3C984D9 CRC64;

Query Match 13.08; Score 711.5; DB 10; Length 692;
Best Local Similarity 28.9%; Pred. No. 3.3e-36;
Matches 199; Conservative 110; Mismatches 252; Indels 127; Gaps 20;

QY 431 LDKETLTLKPEGVVKAQSKKIPLGIGPSPTQSAKKVRKKAENAHNTPLLVLYGSNM 490
Db 60 LVVPKLSISIDE-----EDESEALGG-----KTKVTFYGTQT 92

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QY 491 GTAEGTARDLAD--IAMSKGFAQVAVTLDSHA-----GNLPREGAVLIVTASY-NGHP 540
Db 93 GTAEQFALAEAEKARYEKAQVAVFDLDDYAMEDDDQYEEKLLKTELALFMVATYGDGP 152
QY 541 PDNAKQFVMDLQASADEV--KGVRYSVFGGDKNATWYTKVPAPFADTELAAKGAENIA 598
Db 153 TDNAARYPKVFTGNERGIWLOQLSYGVFGNROY-EHFNKIAKVILDDLLYEQGGKRLV 211
QY 599 DRGEADADDQFEGYEEWRHMSDVAAYFNLDITENSEDNKSTLSLQFVDSAADMLA-- 656
Db 212 PVGLGDDQDIEDFSKAEFLWPELD-----QLLRDEDDVNAPSTPYTAIPEYRLVIH 266
QY 657 -----KMGAFSTNVASKELQOQSGASRSTRHLELEPKEA-SY 694
Db 267 DPSIISVEDKFSLANGVNSFDIHPGCRVNVAVQKELHKAESDRSCIHLFEIDITGTITY 326
QY 695 QEGDHLGVIPRNVGIVNRTARFGLDASQOIRLEAEKEEKLHPLAKTVSVE----- 747
Db 327 ETGDLGLVYAENSEDEIVE-----EAGKLLDKPLDLLFSIHADNEDGT 368
QY 748 -----ELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE--K 786
Db 369 AIGSSLPPPPGPGCTLHTALACYADLLSPKKAALLAALAHASEPSEADRLKFLSSPOGK 428
QY 787 QAYKEQVLAKRLTMELEKYPACEMKFSEFI-ALLPSIRPRYISYSSSPRVDKQASIT 845
Db 429 NEYSHWYNASQSRLLSEMAEFPSAKPLGVFFAAVAPRPPRYISYSSSPRYTNRVHT 488
QY 846 VSVVSGEAWSGYGEYKGIASNYL--AELQEGDTITCF---ISTPQSEFTLPKOPETPLI 899
Db 489 CALVYGPTPG-RIHKGVCSTWKKHVPQDSWAPFVRT--SNFKLPADPSTPII 545
QY 900 MVGPCTGVAPRFGVQARKOLKEQOQSLGEAHLYFGCRSPHEDYLYQBELENAOSEGIT 959
Db 546 MVGPCTGLAPRFGFLQERMAKENGALGPALVFFGCRNRNMDFIYEDELNNFVEQGVIS 605
QY 960 -LHTAFSRMPNPKTYVQHVMEQDGKLLIELLDQGAHYICGDSQMAPAVEATLMKSYA 1018
Db 606 ELIVAFSREGPQ-KEYVQHKMVDRAAEITWISOGYFYVCGDAKGMAVDVHRTLHTIVQ 664
QY 1019 DVHQVSEADARLWLQLEEKRYAKDVW 1046
Db 665 EQGLDSSKTESMVKLQMEGRYLRDVW 692

RESULT 13
Q43235 PRELIMINARY; PRT; 692 AA.
ID Q43235 PRELIMINARY; PRT; 692 AA.
AC Q43235;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADPH-ferrihemoprotein reductase (EC 1.6.2.4).
OS Vicia sativa (Spring vetch) (Tare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3908;
RN [1]
RP SEQUENCE FROM N.A.
RA Benveniste I., Begue-Kirn C., Lesot A., Hasenfratz M., Durst F.;
RT "Isolation and characterization of a cDNA encoding an NADPH-cytochrome
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z26252; CAA81211.1; -
DR HSSP; P00388; Iu92.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding; 1.

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Db      649 GRYLRDVG 656
      ||| :|||
      649 GRYLRDVG 656

RESULT 15
Q9SUM3
ID      Q9SUM3      PRELIMINARY;      PRT;      711 AA.
AC      Q9SUM3;
DT      01-MAY-2000 (TEMBLrel. 13, Created)
DT      01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT      01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE      NADPH-FERRIHEMOXYGENASE reductase (ATR2) (EC 1.6.2.4).
GN      F9N11.60 OR AT4G30210.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Bevan M., Kalicki J., Wohlmann P., Smith A., Bancroft I., Mewes H.W.,
RA      Mayer K.F.X., Lemcke K., Schueller C.;
RL      Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Arabidopsis sequencing project;
RL      Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Kalicki J., Wohlmann P., Smith A., Mewes H.W., Lemcke K.,
RA      Mayer K.F.X.;
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RA      EU Arabidopsis sequencing project;
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A.
RA      Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA      Palm C.J., Theologis A., Ecker J., Davis R.W.;
RL      Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AL109796; CAB52465.1; -
DR      EMBL; AL161576; CAB81014.1; -
DR      EMBL; AF325101; AAK17169.1; -
DR      HSSP; P00388; IAMO.
DR      InterPro; IPR003097; FAD_binding.
DR      InterPro; IPR001094; Flavodoxin_like.
DR      InterPro; IPR001226; Flavodoxin.
DR      InterPro; IPR001709; FPN_cyt_redctse.
DR      InterPro; IPR001433; Oxred_FAD/NAD(P).
DR      Pfam; PF00667; FAD_binding; 1.
DR      Pfam; PF00258; flavodoxin; 1.
DR      Pfam; PF00175; NAD_binding; 1.
DR      PRINTS; PR00369; FLAVODOXIN.
DR      PRINTS; PR00371; PFNCR.
KW      Oxidoreductase.
SQ      SEQUENCE 711 AA; 78927 MW; F0503108EB7F508F CRC64;

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Query Match      13.0%; Score 709; DB 10; Length 711;
Best Local Similarity 28.4%; Pred. No. 4.9e-36;
Matches 190; Conservative 120; Mismatches 264; Indels 96; Gaps 20;

QY      434 KETLTKEGVVYVAKSKIPGLGIPSPSTEQSAKKVKKKAENAHNTPLLVLYGSMGTA 493
DB      81 KRVEPLKP--LVIKPREEDDGG-----RRK-----VTIFFGTGTGTA 116
QY      494 EGTARDLADTAMSKGAP--QVATLDSHAGN-----LPREGAVLIVTASY-NGHPPDN 543
DB      117 EGFKALGEEAKARYEKTRFKIVDLDDYAADDDEYEELKKEDVAFFFLATYGDGEPTDN 176
QY      544 AKQFVWLDOAS--ADEVKGVYRVFGCGDKWATTYQKVPAFIDETLAAKGAENTADRG 601
DB      177 AARFYKWFTEGDRGEWLNKLYGVFLGNROY-EHFNKVKYKVVDDILVEQGAQLVQVG 235

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Search completed: May 29, 2003, 08:30:49  
Job time : 104 secs

